

related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, arterosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth, survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents an ECM-binding fragment of Ang-1 protein.

Sequence 20 AA:

Query Match Similarity 100.0%; Score 106; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-10; Mismatches 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 LCTKKGVLKGGKREEEKPF 20
Db 1 LCTKKGVLKGGKREEEKPF 20

RESULT 2
ID ADS13769 standard; peptide; 20 AA.
AC ADS13769;

XX DT-DEC-2004 (First entry)

XX DE Human Ang-1 protein ECM-binding fragment.

XX Ang-1; extracellular matrix; ECM; angiopoietin; cytotatic; vasotropic; antidiabetic; antiarthritic; cerebroprotective; antiangiogenic; gene therapy; human.

XX Homo sapiens.

XX PN WO2004076650-A2.

XX 10-SEP-2004.

XX PF 27-FEB-2004; 2004WO-US006101.

XX PR 27-FEB-2003; 2003US-0450582P.

XX PA (UPEB-) UNIV PENNSYLVANIA.

XX PI Yu Q;

XX XX WPI: 2004-653413/63.

XX DR N-PGDB; ADS13787.

XX XX DR WPI: 2004-653413/63.

New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischaemia.

Claim 1; SEQ ID NO 1; 114pp; English.

The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischaemia.

Provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving

CC ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage, arterosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth, survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; CC to treat patients with restenosis by inhibiting re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; CC of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents an ECM-binding fragment of Ang-1 protein.

CC The present sequence represents an ECM-binding fragment of Ang-1 protein.

CC The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving

CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of angiopoietin (Ang-1) protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving

CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-

binding fragment of angiopoietin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, atherosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting the re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to BCM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents a linker peptide region of Ang-1 protein.

Sequence 26 AA;

Query Match 100.0%; Score 106; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.e-03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 LCPKBGVLLKGKREEEKF 20
Db 7 LCTKEGVLLKGKREEEKF 26

RESULT 4

AAE32344 standard; protein; 235 AA.
ID: AAE32344
AC: AAE32344;
XX 24-MAR-2003 (first entry)

DE Human angiopoietin-1 (Ang-1) truncated protein #1.
XX Vascular endothelial growth factor; VEGF; angiogenesis; wound healing; bone growth; osteoporosis; osteoarthritis; bone reconstruction; ulcer; lesion; injury; trauma; periodontal condition; protein therapy; human; angiopoietin-1; Ang-1.
XX Homo sapiens.
XX WO200281851-A2.
XX 24-OCT-2002.
XX 10-APR-2002; 2002WO-US011406.
XX 10-APR-2001; 2001US-00832355.

PA (GENV-) GENVEC INC.
XX Kovesdi I, Kessler PD;
XX DR; 2003-075536/07.

XX New fusion protein comprising a non-heparin-binding vascular endothelial growth factor (VEGF) peptide portion and a non-VEGF peptide portion and a non-VEGF peptide portion, useful for promoting angiogenesis and/or bone growth in mammals.
XX Disclosure; Page 126-127; 191pp; English.

binding fragment of angiopoietin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, atherosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting the re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to BCM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents a linker peptide region of Ang-1 protein.

Sequence 235 AA;

Query Match 100.0%; Score 106; DB 6; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 LCTKEGVLLKGKREEEKF 20
Db 215 LCTKEGVLLKGKREEEKF 234

RESULT 5

AD123636 standard; protein; 261 AA.
ID: AD123636
XX AD123636;
AC 22-APR-2004 (first entry)
DE Human Ang-1 fibrinogen-like domain/Preprotrypsin signal.
XX Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal; angiopoietin; coiled-coil domain; cell growth; proliferation; matrix protein; transcription factor; growth factor; secretory protein; cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP; Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell; endothelial precursor cell.
XX Homo sapiens.
OS Synthetic.

KW Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal; angiopoietin; coiled-coil domain; cell growth; proliferation; matrix protein; transcription factor; growth factor; secretory protein; cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP; Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell; endothelial precursor cell.
XX Homo sapiens.
OS Synthetic.
XX US2003220476-A1.
XX 27-NOV-2003.
XX 18-OCT-2002; 2002US-00273180.
XX 21-MAY-2002; 2002US-0382541P.
XX (KOHG/) KOH G Y.
XX Koh GY;
PI Koh GY;
XX WPI; 2004-010889/01.
DR N-PSDB; AD123635.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of ligand or ligand binding domain of a receptor, which forms a biologically active multimer, and where the chimeric molecule in its non-multimeric form is not biologically active. Also included are an isolated nucleic acid encoding the coiled coil chimeric molecule, an expression vector

comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimeric molecule, promoting cell growth or proliferation, and making a chimeric inhibiting ligand activity or cell proliferation, and making a chimeric molecule. The coiled coil chimeric molecule comprises a domain belonging to a matrix protein family, transcription factor family, growth factor family or secretory protein family. The coiled coil domain is from cartilage matrix protein (COMP) or cartilage oligomeric matrix protein (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -2, -3 or -4. The chimeric molecules are useful for promoting or inhibiting a differential function and/or influencing the phenotype, such as growth, survival, contractility, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibrinogen-like domain of Ang-1 with a proptrypsin leader.

Sequence 261 AA;

Query Match 100.0%; Score 106; DB 8; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.4e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 139 LCTKEGVNLKGGRKEEKF 20

AD123638 standard; protein; 298 AA.

RESULT 6

AD123638

ID AD123638

AC AD123638;

XX DT 22-APR-2004 (first entry)

XX XX

XX Yeast Gcn4 coiled-coil domain/Human Ang-1 cDNA.

XX KW Human; Ang-1; fibrinogen-like domain; Proptrypsin signal;

KW angiopoietin; coiled-coil domain; cell growth; proliferation;

KW matrix protein; transcription factor; growth factor; secretory protein;

KW cartilage matrix protein; COMP; cartilage oligomeric matrix protein; COMP;

KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;

KW endothelial precursor cell; yeast.

XX OS Homo sapiens.

OS Saccharomyces cerevisiae.

OS Chimeric.

XX PN US2003220476-A1.

XX PD 27-NOV-2003.

XX PF 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PR 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

PI PA (KOHG/) KOH G Y.

XX DR WPI; 2004-010889/01.

DR N-PSDB; AD123637.

XX PT New coiled coil chimeric molecule comprising a coiled-coil domain linked

PT to either a receptor binding domain of ligand or ligand binding domain of

PT a receptor, useful for inhibiting or promoting differential function.

PS Example 5; SEQ ID NO 4; 38pp; English.

XX The invention relates to a coiled coil chimeric molecule comprising a

CC coiled-coil domain linked to either a receptor binding domain of a ligand

CC or ligand binding domain of a receptor, which forms a biologically active

coiled-coil domain of Ang-1 with a proptrypsin leader. The present sequence represents the fibrinogen-like domain of Ang-1 in a chimeric protein with a coiled-coil domain.

XX SQ Sequence 298 AA;

Query Match 100.0%; Score 106; DB 8; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.6e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVNLKGGRKEEKF 20

Db 64 LCTKEGVNLKGGRKEEKF 83

RESULT 7

AD123640

ID AD123640 standard; protein; 310 AA.

XX AC AD123640;

XX DT 22-APR-2004 (first entry)

XX DE Human CMP coiled-coil domain/Ang-1.

XX KW Human; Ang-1; fibrinogen-like domain; Preptrypsin signal;

KW angiopoietin; coiled-coil domain; cell growth; proliferation;

KW matrix protein; transcription factor; growth factor; secretory protein;

KW cartilage matrix protein; COMP; cartilage oligomeric matrix protein; COMP;

KW angiopoietin; coiled-coil domain; cell growth; proliferation;

KW matrix protein; transcription factor; growth factor; secretory protein;

KW cartilage matrix protein; COMP; cartilage oligomeric matrix protein; COMP;

KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;

KW endothelial precursor cell.

XX OS Homo sapiens.

OS Synthetic.

XX PN US2003220476-A1.

XX PD 27-NOV-2003.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

PI PA (KOHG/) KOH G Y.

XX DR WPI; 2004-010889/01.

DR N-PSDB; AD123639.

XX PT New coiled coil chimeric molecule comprising a coiled-coil domain linked

PT to either a receptor binding domain of ligand or ligand binding domain of

PT a receptor, useful for inhibiting or promoting differential function.

PS Example 6; SEQ ID NO 6; 38pp; English.

XX The invention relates to a coiled coil chimeric molecule comprising a

CC coiled-coil domain linked to either a receptor binding domain of a ligand

CC or ligand binding domain of a receptor, which forms a biologically active

CC The invention relates to a coiled coil chimaeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of a ligand or ligand binding domain of a receptor, which forms a biologically active multimer, and where the chimaeric molecule in its non-multimeric form is not biologically active. Also included are in isolated nucleic acid encoding the coiled coil chimaeric molecule, an expression vector comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimaeric molecule, promoting cell growth or proliferation, decreasing or inhibiting ligand activity or cell proliferation and making a chimaeric molecule. The coiled coil chimaeric molecule comprises a domain belonging to a matrix protein family, transcription factor family, growth factor matrix or secretory protein family. The coiled coil domain is from cartilage matrix protein (CMP) or cartilage oligomeric matrix protein (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -2, -3 or -4. The chimaeric molecules are useful for promoting or inhibiting differential function and/or influencing the phenotype, such as growth, survival, contraction, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-coil domain.

XX Sequence 310 AA;

Query Match 100.0%; Score 106; DB 8; Length 310;

Best Local Similarity 100.0%; Pred. No. 1.7e-08; NMatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; NMatches 0; Indels 0; Gaps 0;

Qy 1 LCTREGVLLKGKGKREBKEPF 20

Db 76 LCTREGVLLKGKGKREBKEPF 95

RESULT 8
ID ADI23642
ID ADI23642 standard; protein; 312 AA.

XX AC AAE38503;
XX DT 22-APR-2004 (first entry)
XX DE Human COMP coiled-coil domain/Ang-1.
XX Human; Ang-1; fibrinogen-like domain; Preprotryptin signal; angiopoietin1; coiled-coil domain; cell growth; proliferation; matrix protein; transcription factor; growth factor; secretory protein; cartilage matrix protein; CMP; cartilage oligomeric matrix protein; Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell; endothelial precursor cell.
XX Homo sapiens.
XX Synthetic.

OS OS2003220476-A1.
XX PD 27-NOV-2003.
XX PP 18-OCT-2002; 2002US-00273180.
XX PR 21-MAY-2002; 2002US-0382541P.
XX PA (KORG/) KOH G Y.
XX PI Koh GY;

XX DR WPI; 2004-010889/01.
XX DR N-PSDB; ADI23641.
XX PT New coiled coil chimeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of ligand or ligand binding domain of a receptor, useful for inhibiting or promoting differential function.

XX Example 7; SEQ ID NO 8; 38pp; English.
PS The invention relates to a coiled coil chimaeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of a ligand or ligand binding domain of a receptor, which forms a biologically active multimer, and where the chimaeric molecule in its non-multimeric form is not biologically active. Also included are in isolated nucleic acid encoding the coiled coil chimaeric molecule, an expression vector comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimaeric molecule, promoting cell growth or proliferation, decreasing or inhibiting ligand activity or cell proliferation and making a chimaeric molecule. The coiled coil chimaeric molecule comprises a domain belonging to a matrix protein family, transcription factor family, growth factor family or secretory protein family. The coiled coil domain is from cartilage matrix protein (CMP) or cartilage oligomeric matrix protein (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -2, -3 or -4. The chimaeric molecules are useful for promoting or inhibiting a differential function and/or influencing the phenotype, such as growth, survival, contractility, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-coil domain.

XX SQ Sequence 312 AA;

Query Match 100.0%; Score 106; DB 8; Length 312;

Best Local Similarity 100.0%; Pred. No. 1.7e-08; NMatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; NMatches 0; Indels 0; Gaps 0;

Qy 1 LCTREGVLLKGKGKREBKEPF 20

Db 78 LCTREGVLLKGKGKREBKEPF 97

RESULT 9
AAE38503
ID AAE38503 standard; protein; 402 AA.
XX AC AAE38503;
XX DT 20-NOV-2003 (first entry)
XX DE Human angiopoietin-1 #4.
XX Human angiopoietin-1 #4.
XX KW Angiopoietin-1; endothelium; cell proliferation; tumour; gene therapy;
KW Angiopoietin-1; endothelium; cell proliferation; tumour.
KW human.
XX Homo sapiens.

OS OS200308165-A2.
XX PN WO200308165-A2.
XX DT 21-AUG-2003.
XX PD 14-FEB-2003; 2003WO-US04595.
XX PR 14-FEB-2002; 2002US-0356809P.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Ellis LM;
XX DR WPI; 2003-697465/66.
XX PT Stabilizing the endothelium or reducing endothelial cell proliferation associated with a tumor comprises administering to a patient having a tumor angiopoietin-1 polypeptide.

XX PT
XX PS Disclosure; Page 139-140; 157pp; English.

Page 6

The invention relates to a method for stabilising the endothelium or reducing endothelial cell proliferation associated with a tumour by administering angiopoietin-1 polypeptide to a patient having tumour. The method is useful for stabilising the endothelium or reducing endothelial cell proliferation associated with a tumour. It is also useful in gene therapy. The present sequence is human angiopoietin-1. This sequence is used to illustrate the method of the invention.

C The invention relates to a method for stabilising the endothelium or
 C reducing endothelial cell proliferation associated with a tumour by
 C administering angiopoietin-1 polypeptide to a patient having tumour. The
 C method is useful for stabilising the endothelium or reducing endothelial
 C cell proliferation associated with a tumour. It is also useful in Gene
 C therapy. The present sequence is human angiopoietin-1. This sequence is
 C used to illustrate the method of the invention
 X Sequence 402 AA;
 X
 Query Match 100.0%; Score 106; DB 7; Length 402;
 Best Local Similarity 100.0%; Pred. No. 2.2e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 LCTKEGVLLKGKREEEKPP 20
 Y 264 LCTKEGVLLKGKREEEKPP 283
 Q
 Qy 1 LCTKEGVLLKGKREEEKPP 20
 Qy 264 LCTKEGVLLKGKREEEKPP 283
 Db 1 LCTKEGVLLKGKREEEKPP 20
 Db 264 LCTKEGVLLKGKREEEKPP 283
 Result 11
 ADS13776 ADS13776 standard; protein: 456 AA.
 XX
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 AC ADS13776;
 AC ADS13776;
 DT 02-DEC-2004 (first entry)
 DE Mouse Ang-1 protein non-ECM-binding fragment.
 XX
 XX
 KW Arg-1; extracellular matrix; ECM; angiopoietin; cytotatic; vasoconstrictive;
 KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
 KW gene therapy; mouse

18 Homo sapiens.
 19 US2005136455-A1.
 20 23-JUN-2005.
 21 22-DEC-2004; 2004US-00019829.
 22 22-DEC-2003; 2003BP-00104902.
 23 (CLERC R. G.
 24 (DUCHATEAU-NGUYEN G.
 25 (GARDÉS C.
 26 (MIZRAHI J.
 27 (OSTENSON C.
 28 Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;
 29 WPI: 2005-457507/46.
 30 N-PSDB; AEA81187.
 31 Screening test compounds that reduce and/or prevent obesity involves
 32 contacting cell expressing gene from alpha-two-glycoprotein.
 33 Claim 20; SEQ ID NO 115; 21pp; English.
 34 The invention relates to a novel method for screening for test compounds
 35 that reduce and/or prevent obesity. The method comprises contacting a
 36 cell expressing gene from alpha-two-glycoprotein with a test compound
 37 and measuring the effect of the test compound on the cell. The invention
 38 also relates to a pharmaceutical composition comprising a pharmaceutical carrier and an
 39 amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
 40 or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
 41 ischaemia.
 42 XX WPI: 2004-653413/63.
 43 DR N-PSDB; ADS13794.
 44 XX PT
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CC compound. The method of the invention demonstrates anorectic applications
 CC and may be useful for screening for compounds that reduce and/or prevent
 CC obesity. The current sequence is that of the human angiopoietin 1
 CC (ANGPT1), transcript variant 2 protein of the invention. The sequence
 CC listing for the specification can be located via the USPRO web-site.
 CC
 CC Sequence 402 AA:
 CC
 CC Query Match 100.0%; Score 106; DB 9; Length 402;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e-08;
 CC Mismatches 0; Indels 0; Gaps 0;
 CC March 20: Conservative 0;
 CC Mismatches 0; Indels 0; Gaps 0;
 CC Sequence 456 AA:
 CC SO
 CC
 CC

Query Match 100.0%; Score 106; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRBEEKPF 20
Db 222 LCTKEGVLLKGKGRBEEKPF 241

RESULT 1.2
ADS13775 standard; protein; 456 AA.
XX
AC ADS13775
XX
DT 02-DEC-2004 (first entry)
XX Human Ang-1 protein non-ECM-binding fragment.
DE AAM47526;
XX KW extracellular matrix; ECM; angiopoietin; cytostatic; vasotropin;
KW antidiabetic; antiarthritic; cerebroprotective;
gene therapy; human.
XX
OS Homo sapiens.
PN WO2004076650-A2.
XX
PD 10-SEP-2004.
XX
PP 27-FEB-2004; 2004W0-US006101.
XX
PR 27-FEB-2003; 2003US-0450582P.
XX
PA (TYPE-) UNIV PENNSYLVANIA.
XX
PI Yu Q;
XX
DR 2004-653413/53.
DR N-PDBB; ADS13793.
XX
PR New pharmaceutical composition comprises a pharmaceutical carrier and an
PT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
PT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
PT ischaemia.
XX
PS Claim 5; SEQ ID NO 7; 114pp; English.
XX
CC The invention relates to a pharmaceutical composition comprising a
pharmaceutical carrier and an amount of an extracellular matrix (ECM)-
binding fragment of angiopoietin (Ang-1) protein or a mutant Ang-1. Also
provided are methods of treating an individual suspected of having
coronary artery disease, vascular disease or a condition involving
ischaemia; of promoting angiogenesis, endothelial survival and
maintaining vascular integrity in an individual; of treating an
individual suspected of having a disease related to lack of blood vessels
to effectively promote angiogenesis in the patients with the diseases
related to lack of blood vessels such as ischaemia in hearts and limbs;
to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
atherosclerosis risk by maintaining the health and integrity of blood
vessels; to assist the recovery of the patients who had stroke and the
angioplasty procedure by promoting the growth/survature of endothelial
cells and establish endothelial monolayer and inhibit excessive
inflammation, haemorrhage, and proliferation of vascular smooth muscle;
CC to treat patients with restenosis by inhibiting re-closure of blood
vessel after inserting stents into blood vessels; to make stable and
functional artificial blood vessels comprising using the composition
above; of identifying compounds that modulates binding of Ang-1 to ECM;
CC of treating an individual suspected of having cancer; of preventing
diabetes and/or arthritis in an individual suspected of being at risk of
developing diabetes or arthritis. The pharmaceutic composition is
useful for treating diseases and disorders, e.g. cancer, coronary artery
disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
CC angiogenesis, or arthritis. The present sequence represents a non-ECM-
binding fragment of Ang-1 protein.
XX
SQ Sequence 456 AA;

Query Match 100.0%; Score 106; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRBEEKPF 20
Db 222 LCTKEGVLLKGKGRBEEKPF 241

RESULT 1.3
AAM47526 standard; protein; 494 AA.
XX
AC AAM47526;
XX
DT 09-SEP-1998 (first entry)
XX Amino acid sequence of chimeric TIE ligand 2N1C1F (chimera 4).
DE Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation; tumour;
KW human.
XX
OS Homo sapiens.
XX
PN WO9805779-A1.
XX
PD 12-FEB-1998.
XX
PP 01-AUG-1997; 97WO-US013557.
XX
PR 02-AUG-1996; 96US-0022999P.
PR 25-OCT-1996;
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Davis S, Yancopoulos GD;
XX
DR WPI; 1998-145615/13.
DR N-PDBB; AAV18613.
XX
PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
PT healing.
XX
PS Claim 20; Fig 27; 202pp; English.

CC This is the amino acid sequence of the chimeric TIE ligand 2N1C1F, used
in the method of the invention, involving the production of TIE-2 ligands
which promote healing. The nucleic acids, vectors and host cells used in
the method of the invention are useful for the recombinant production of
the ligands. The ligands, etc. are useful for blocking blood vessel
growth, promoting neovascularisation, promoting the growth or
differentiation of a cell expressing the TIE receptor, blocking the
growth or differentiation of a cell expressing the TIE receptor and for
attenuating or preventing tumour growth in a human
CC
XX
SQ Sequence 494 AA;

Query Match 100.0%; Score 106; DB 2; Length 494;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRBEEKPF 20
Db 260 LCTKEGVLLKGKGRBEEKPF 279

RESULT 1.4
AAR94603 standard; protein; 498 AA.
ID AAR94603

XX AAR94603;
 XX DT 28-OCT-1996 (first entry)
 XX DB Human TIE-2 ligand 1 derived from lambda-gt10 clone.
 XX KW Angiogenesis; neovascularisation; tumour development; wound healing; TIE;
 XX tyrosine kinase with Ig and EGF homology domains; vector; recombinant;
 XX clone; diagnosis; ischaemia; thromboembolic disease; atherosclerosis;
 XX inflammation; diabetes; ligand bodies; delivery; targeting.
 OS Homo sapiens.
 XX PH Key
 FT Modified-site 269
 FT /note= "extra Gly residue not present in TIE-2 ligand 1
 derived from T98G clone (see AAT14649 and AAR94604)"
 XX PN WO9611269-A2.
 XX PD 18-APR-1996.
 XX PF 06-OCT-1995;
 XX 95WO-US012935.
 XX PR 07-OCT-1994;
 XX 94US-00319932.
 XX PR 27-OCT-1994;
 XX 94US-00310261.
 XX PR 02-DEC-1994;
 XX 94US-00348992.
 XX PR 09-DEC-1994;
 XX 94US-00353503.
 XX PR 17-JAN-1995;
 XX 95US-00373579.
 XX PR 06-APR-1995;
 XX 95US-00418595.
 PA (REGEB-) REGENERON PHARM INC.
 XX PI Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisonpierre PC;
 PI Radziejewski C, Jones PF, Yancopoulos GD;
 XX WPI; 1996-209850/21.
 DR N-PPDB; AAT14648.
 XX PT Nucleic acid encoding TIE-2 ligand and related vectors - useful in
 PT diagnosis and treatment of neovascularisation, tumours, etc., or to
 PT promote wound healing, etc.
 PS XX Claim 2: Fig 4; 84PP; English.
 XX AAR94603 is a recombinant human TIE-2 (hTIE-2) ligand 1 derived from a
 CC lambda-gt10 clone. The ligand has an extra Gly residue (aa 269) as
 CC compared to the hTIE-2 ligand from T98G clone (see AAT1649 and
 CC AAR94604). hTIE-2 ligand DNAs of the invention are recombinant versions
 CC of the native ligand coding sequences and may be used to produce the
 CC ligands at a high yield. Antibodies and receptor bodies that bind to TIE-
 CC 2 ligands may be used to inhibit angiogenesis and neovascularisation
 CC (e.g. associated with tumour development) and the TIE-2 ligands
 CC themselves are useful to promote neovascularisation and wound healing
 CC (e.g. for treatment of ischaemia, thromboembolic disease, inflammation and diabetes).
 CC Ligand bodies (contg. TIE-2 ligands may also be useful for the delivery
 CC and targeting of growth factors, toxins etc. to sites where their
 CC presence is advantageous
 XX Sequence 498 AA;
 SQ Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Gaps 0;
 Qy 1 LCTKEGVLLKGKGRBEEKPF 20
 Db 264 LCTKEGVLLKGKGRBEEKPF 283
 Search completed: December 29, 2005, 15:36:17
 Job time : 186 secs

| Result No. | Score | Query | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|-------------------|--------------------|-------------|
| 1 | 106 | 100.0 | 478 | 2 | US-08-740-223A-7 | Sequence 7, Appli | |
| 2 | 106 | 100.0 | 478 | 2 | US-09-709-188-7 | Sequence 7, Appli | |
| 3 | 106 | 100.0 | 478 | 2 | US-10-225-060-7 | Sequence 7, Appli | |
| 4 | 106 | 100.0 | 495 | 2 | US-08-740-223A-26 | Sequence 26, Appli | |
| 5 | 106 | 100.0 | 495 | 2 | US-09-709-188-26 | Sequence 26, Appli | |
| 6 | 106 | 100.0 | 495 | 2 | US-10-225-060-26 | Sequence 26, Appli | |
| 7 | 106 | 100.0 | 497 | 2 | US-08-740-223A-14 | Sequence 14, Appli | |
| 8 | 106 | 100.0 | 497 | 2 | US-09-709-188-14 | Sequence 14, Appli | |
| 9 | 106 | 100.0 | 497 | 2 | US-10-225-060-14 | Sequence 2, Appli | |
| 10 | 106 | 100.0 | 498 | 1 | US-08-373-579-2 | Sequence 2, Appli | |
| 11 | 106 | 100.0 | 498 | 1 | US-08-418-595-2 | Sequence 2, Appli | |
| 12 | 106 | 100.0 | 498 | 1 | US-08-665-926-2 | Sequence 2, Appli | |
| 13 | 106 | 100.0 | 498 | 1 | US-08-349-492-2 | Sequence 2, Appli | |
| 14 | 106 | 100.0 | 498 | 2 | US-09-162-337-2 | Sequence 2, Appli | |
| 15 | 106 | 100.0 | 498 | 2 | US-08-740-223A-2 | Sequence 2, Appli | |
| 16 | 106 | 100.0 | 498 | 2 | US-08-740-223A-20 | Sequence 2, Appli | |
| 17 | 106 | 100.0 | 498 | 2 | US-09-351-557-2 | Sequence 2, Appli | |
| 18 | 106 | 100.0 | 498 | 2 | US-09-561-100-2 | Sequence 2, Appli | |
| 19 | 106 | 100.0 | 498 | 2 | US-09-561-108-2 | Sequence 2, Appli | |
| 20 | 106 | 100.0 | 498 | 2 | US-09-551-543-2 | Sequence 2, Appli | |
| 21 | 106 | 100.0 | 498 | 2 | US-09-526-2 | Sequence 2, Appli | |
| 22 | 106 | 100.0 | 498 | 2 | US-09-202-491-5 | Sequence 5, Appli | |
| 23 | 106 | 100.0 | 498 | 2 | US-09-202-491-6 | Sequence 6, Appli | |
| 24 | 106 | 100.0 | 498 | 2 | US-08-817-318-2 | Sequence 2, Appli | |
| 25 | 106 | 100.0 | 498 | 2 | US-09-188-188-2 | Sequence 2, Appli | |
| 26 | 106 | 100.0 | 498 | 2 | US-09-109-188-20 | Sequence 2, Appli | |
| 27 | 106 | 100.0 | 498 | 2 | US-09-561-499-2 | Sequence 2, Appli | |

GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 29, 2005, 15:32:59 ; Search time 46 Seconds
(without alignments)
35.946 Million cell updates/secTitle: US-10-789-222-1
Perfect score: 106
Sequence: 1 LCTKEGVLLKGKRRBBKPF 20Scoring table: BIOSUM62
Gapext 0.5
Scoring: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6/pbodata/1/iaa/5_COMB.pep:
 2: /cgn2_6/pbodata/1/iaa/6_COMB.pep:
 3: /cgn2_6/pbodata/1/iaa/H_COMB.pep:
 4: /cgn2_6/pbodata/1/iaa/PTUS_COMB.pep:
 5: /cgn2_6/pbodata/1/iaa/RE_COMB.pep:
 6: /cgn2_6/pbodata/1/iaa/backfile1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|-------------------|--------------------|-------------|
| 1 | 106 | 100.0 | 478 | 2 | US-08-740-223A-7 | Sequence 7, Appli | |
| 2 | 106 | 100.0 | 478 | 2 | US-09-709-188-7 | Sequence 7, Appli | |
| 3 | 106 | 100.0 | 478 | 2 | US-10-225-060-7 | Sequence 7, Appli | |
| 4 | 106 | 100.0 | 495 | 2 | US-08-740-223A-26 | Sequence 26, Appli | |
| 5 | 106 | 100.0 | 495 | 2 | US-09-709-188-26 | Sequence 26, Appli | |
| 6 | 106 | 100.0 | 495 | 2 | US-10-225-060-26 | Sequence 26, Appli | |
| 7 | 106 | 100.0 | 497 | 2 | US-08-740-223A-14 | Sequence 14, Appli | |
| 8 | 106 | 100.0 | 497 | 2 | US-09-709-188-14 | Sequence 14, Appli | |
| 9 | 106 | 100.0 | 497 | 2 | US-10-225-060-14 | Sequence 2, Appli | |
| 10 | 106 | 100.0 | 498 | 1 | US-08-373-579-2 | Sequence 2, Appli | |
| 11 | 106 | 100.0 | 498 | 1 | US-08-418-595-2 | Sequence 2, Appli | |
| 12 | 106 | 100.0 | 498 | 1 | US-08-665-926-2 | Sequence 2, Appli | |
| 13 | 106 | 100.0 | 498 | 1 | US-08-349-492-2 | Sequence 2, Appli | |
| 14 | 106 | 100.0 | 498 | 2 | US-09-162-337-2 | Sequence 2, Appli | |
| 15 | 106 | 100.0 | 498 | 2 | US-08-740-223A-2 | Sequence 2, Appli | |
| 16 | 106 | 100.0 | 498 | 2 | US-08-740-223A-20 | Sequence 2, Appli | |
| 17 | 106 | 100.0 | 498 | 2 | US-09-351-557-2 | Sequence 2, Appli | |
| 18 | 106 | 100.0 | 498 | 2 | US-09-561-100-2 | Sequence 2, Appli | |
| 19 | 106 | 100.0 | 498 | 2 | US-09-561-108-2 | Sequence 2, Appli | |
| 20 | 106 | 100.0 | 498 | 2 | US-09-551-543-2 | Sequence 2, Appli | |
| 21 | 106 | 100.0 | 498 | 2 | US-09-526-2 | Sequence 2, Appli | |
| 22 | 106 | 100.0 | 498 | 2 | US-09-202-491-5 | Sequence 5, Appli | |
| 23 | 106 | 100.0 | 498 | 2 | US-09-202-491-6 | Sequence 6, Appli | |
| 24 | 106 | 100.0 | 498 | 2 | US-08-817-318-2 | Sequence 2, Appli | |
| 25 | 106 | 100.0 | 498 | 2 | US-09-188-188-2 | Sequence 2, Appli | |
| 26 | 106 | 100.0 | 498 | 2 | US-09-109-188-20 | Sequence 2, Appli | |
| 27 | 106 | 100.0 | 498 | 2 | US-09-561-499-2 | Sequence 2, Appli | |

ALIGNMENTS

RESULT 1
 US-08-740-223A-7
 ; Sequence 7, Application US/08740223A
 ; Patent No. 6265164
 ; GENERAL INFORMATION:
 ; APPLICANT: David, et al.
 ; TITLE OF INVENTION: Expressed Ligand - Vascular
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 ; STREET: 777 Old Saw Mill Road
 ; CITY: Tarrytown
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10591
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/740-223A
 ; FILING DATE: 25-OCT-1996
 ; CLASSIFICATION: 536
 ; PRIORITY APPLICATION NUMBER: USSN 60/022/999
 ; APPLICATION NUMBER: USSN 60/022/999
 ; FILING DATE: 02-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cober, Robert J.
 ; REGISTRATION NUMBER: 36,108
 ; REFERENCE/DOCKET NUMBER: REG 333
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 914-345-7400
 ; TELEFAX: 914-345-7711
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 478 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Mature TLLI protein
 ; LOCATION: 1..478
 ; OTHER INFORMATION:
 ; US-08-740-223A-7
 ; Query Match Best Local Similarity 100.0% ; Score 106 ; DB 2 ; Pred. No. 3.ee-09 ; Length 478;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; /
 Qy 1 LCTKEGVLLKGKGRREBKKP 20 /
 Db 244 LCTKEGVLLKGKGRREBKKP 263 /

RESULT 2
 US-09-709-188-7
 Sequence 7, Application US/09709188
 Patent No. 6441137 /
 GENERAL INFORMATION:
 APPLICANT: Davis et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
 FILE REFERENCE: REG 333-2
 CURRENT APPLICATION NUMBER: US/09/709,188
 CURRENT FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: US/08/740,223
 PRIOR FILING DATE: 1996-10-25
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 7
 LENGTH: 478
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-709-188-7

Query Match 100.0%; Score 106; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 3.2e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; /
 Qy 1 LCTKEGVLLKGKGRREBKKP 20
 Db 244 LCTKEGVLLKGKGRREBKKP 263

RESULT 3
 US-10-225-060-7
 Sequence 7, Application US/10225060
 Patent No. 6625008 /
 GENERAL INFORMATION:
 APPLICANT: Davis et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
 FILE REFERENCE: REG 333-2
 CURRENT APPLICATION NUMBER: US/10/225,060
 CURRENT FILING DATE: 2002-08-21
 PRIOR APPLICATION NUMBER: US/09/709,188
 PRIOR FILING DATE: 2000-11-09
 PRIOR FILING DATE: 1996-10-25
 NUMBER OF SEQ ID NOS: 30
 SEQ ID NO 7
 LENGTH: 478
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-225-060-7

Query Match 100.0%; Score 106; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 3.2e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; /
 Qy 1 LCTKEGVLLKGKGRREBKKP 20
 Db 244 LCTKEGVLLKGKGRREBKKP 263

RESULT 4
 US-08-740-223A-26
 Sequence 26, Application US/08740223A
 Patent No. 6255564 /
 GENERAL INFORMATION:
 APPLICANT: Davis et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
 FILE REFERENCE: REG 333-2
 CURRENT APPLICATION NUMBER: US/09/709,188
 CURRENT FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: US/08/740,223
 PRIOR FILING DATE: 1996-10-25
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 26
 LENGTH: 495
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATUE: /
 OTHER INFORMATION: Description of Artificial Sequence: Chimeric

RESULT 5
 US-09-709-188-26
 Sequence 26, Application US/09709188
 Patent No. 6441137 /
 GENERAL INFORMATION:
 APPLICANT: Davis et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
 FILE REFERENCE: REG 333-2
 CURRENT APPLICATION NUMBER: US/09/709,188
 CURRENT FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: US/08/740,223
 PRIOR FILING DATE: 1996-10-25
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 26
 LENGTH: 495
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATUE: /
 OTHER INFORMATION: Description of Artificial Sequence: Chimeric

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Sequence 2, Application US/08665926
Patent No. 5851797
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Covert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-926-2

Query Match          100.0%;  Score 106;  DB 1;  Length 498;
Best Local Similarity 100.0%;  Pred. No. 3.3e-09;
Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;
Oy          1 LCTKEGVLLKGGRREEKPF 20
Db          264 LCTKEGVLLKGGRREEKPF 283

RESULT 13
US-08-348-492-2
Sequence 2, Application US/08348492
Patent No. 5873672
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,492
FILING DATE: 02-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kempfer, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 330B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 347-7000
TELEFAX: (914) 347-2113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-432-2

Query Match          100.0% Score 1
Best Local Similarity 100.0% Pred. Mismatches 0; Mismatches 0;
Matches 20; Conservative 0;

Qy      1 LCTKEGVLLIKGGKREBEPF 20
Db      264 LCTKEGVLLIKGGKREBEPF 283

RESULT 14
US-09-162-437-2
Sequence 2, Application US/09162437
Patent No. 6166185
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIB-2 LIGAND, MU
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEES: Regeneron Pharmaceuticals
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,437
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418,595
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.

```

REGISTRATION NUMBER: 36.108
 REFERENCE/DOCKET NUMBER: REG 330-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 345-7400
 TELEFAX: (914) 345-7721
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-162-437-2

Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGGKREEKPP 20
 Db 264 LCTKEGVLLKGKGGKREEKPP 283

Search completed: December 29, 2005, 15:41:47
 Job time : 47 secs

RESULT 15
 US-08-740-223A-2
 Sequence 2, Application US/08740223A
 Patent No. 6265564

GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular
 TITLE OF INVENTION: Intercellular Signalling Molecule
 NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill Road
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/740,223A
 FILING DATE: 25-OCT-1996

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USIN 60/022/999
 FILING DATE: 02-AUG-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Cobert, Robert J
 REGISTRATION NUMBER: 36,108
 REFERENCE/DOCKET NUMBER: REG 333

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 914-345-7400
 TELEFAX: 914-345-7721

SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Human TIE-2 ligand 1
 LOCATION: 1..:498
 OTHER INFORMATION: from clone gtl0 encoding hr1e-2
 OTHER INFORMATION: ligand 1

US-08-740-223A-2

Query Match 100.0%; Score 106; DB 2; Length 498;

| Result | No. | Score | Query | Match | Length | DB | ID | Description |
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| 2 | 2 | 106 | 100.0 | 20 | 4 | US-10-789-222-1 | Sequence 2, Appli | ; Sequence 1, Application US/10789222 |
| 3 | 3 | 106 | 100.0 | 235 | 3 | US-09-832-355A-18 | Sequence 18, Appli | ; Publication No. US20040186054A1 |
| 4 | 4 | 106 | 100.0 | 260 | 4 | US-10-273-180-2 | Sequence 2, Appli | ; GENERAL INFORMATION: |
| 5 | 5 | 106 | 100.0 | 298 | 4 | US-10-273-180-4 | Sequence 4, Appli | ; APPLICANT: YU, QIN |
| 6 | 6 | 106 | 100.0 | 309 | 4 | US-10-273-180-6 | Sequence 6, Appli | ; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses |
| 7 | 7 | 106 | 100.0 | 312 | 4 | US-10-273-180-8 | Sequence 8, Appli | ; FILE REFERENCE: UPN0003-100 (P3115) |
| 8 | 8 | 106 | 100.0 | 402 | 6 | US-11-019-829-11-15 | Sequence 36, Appli | ; CURRENT APPLICATION NUMBER: US/10789222 |
| 9 | 9 | 106 | 100.0 | 402 | 6 | US-11-019-829-11-15 | Sequence 7, Appli | ; PRIORITY FILING DATE: 2004-02-27 |
| 10 | 10 | 106 | 100.0 | 456 | 4 | US-10-789-222-7 | Sequence 26, Appli | ; PRIOR APPLICATION NUMBER: US 60/450,582 |
| 11 | 11 | 106 | 100.0 | 456 | 4 | US-10-789-222-8 | Sequence 26, Appli | ; PRIORITY FILING DATE: 2003-02-27 |
| 12 | 12 | 106 | 100.0 | 478 | 4 | US-10-225-060-14 | Sequence 7, Appli | ; NUMBER OF SEQ ID NOS: 36 |
| 13 | 13 | 106 | 100.0 | 478 | 5 | US-10-928-911-7 | Sequence 7, Appli | ; SOFTWARE: PatentIn version 3.2 |
| 14 | 14 | 106 | 100.0 | 478 | 6 | US-11-073-120-7 | Sequence 7, Appli | ; SEQ ID NO 1 |
| 15 | 15 | 106 | 100.0 | 495 | 4 | US-10-225-060-26 | Sequence 26, Appli | ; LENGTH: 20 |
| 16 | 16 | 106 | 100.0 | 495 | 5 | US-10-928-911-26 | Sequence 26, Appli | ; TYPE: PRT |
| 17 | 17 | 106 | 100.0 | 495 | 6 | US-11-073-120-26 | Sequence 26, Appli | ; ORGANISM: Homo sapiens |
| 18 | 18 | 106 | 100.0 | 497 | 4 | US-10-225-060-14 | Sequence 14, Appli | ; SEQ ID NO 2 |
| 19 | 19 | 106 | 100.0 | 497 | 5 | US-10-928-911-14 | Sequence 14, Appli | ; LENGTH: 20 |
| 20 | 20 | 106 | 100.0 | 497 | 6 | US-11-073-120-14 | Sequence 14, Appli | ; TYPE: PRT |
| 21 | 21 | 106 | 100.0 | 498 | 3 | US-09-998-831-2 | Sequence 2, Appli | ; ORGANISM: mouse |
| 22 | 22 | 106 | 100.0 | 498 | 3 | US-09-998-831-2 | Sequence 13, Appli | ; SEQ ID NO 3 |
| 23 | 23 | 106 | 100.0 | 498 | 3 | US-09-832-355A-15 | Sequence 15, Appli | ; LENGTH: 20 |
| 24 | 24 | 106 | 100.0 | 498 | 3 | US-09-998-833-2 | Sequence 2, Appli | ; TYPE: PRT |
| 25 | 25 | 106 | 100.0 | 498 | 4 | US-10-179-744-2 | Sequence 2, Appli | ; ORGANISM: mouse |
| 26 | 26 | 106 | 100.0 | 498 | 4 | US-10-186-177-2 | Sequence 5, Appli | ; SEQ ID NO 4 |
| 27 | 27 | 106 | 100.0 | 498 | 4 | US-10-215-224-5 | Sequence 5, Appli | ; LENGTH: 20 |

ALIGNMENTS

Query Match 100.0%; Score 106; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e-09; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 SEQ ID NO: 1 LCTKEGVLLKGKGKREBKEPF 20
 Db 1 LCTKEGVLLKGKGKREBKEPF 20

RESULT 3
 US-09-832-355A-18
 Sequence 18, Application US/09832355A
 Publication No. US2003027751A1
 GENERAL INFORMATION:
 APPLICANT: Kovacs, Imre
 APPLICANT: Kessler, Paul
 TITLE OF INVENTION: VEGF FUSION PROTEINS
 FILE REFERENCE: 205654
 CURRENT APPLICATION NUMBER: US/09/832,355A
 CURRENT FILING DATE: 2001-04-10
 NUMBER OF SEQ ID NOS: 126
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 18
 LENGTH: 235
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-832-355A-18

Query Match 100.0%; Score 106; DB 3; Length 235;
 Best Local Similarity 100.0%; Pred. No. 2.2e-08; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 SEQ ID NO: 1 LCTKEGVLLKGKGKREBKEPF 20
 Db 1 LCTKEGVLLKGKGKREBKEPF 234

RESULT 4
 US-10-273-180-2
 Sequence 2, Application US/10273180
 Publication No. US20030220476A1
 GENERAL INFORMATION:
 APPLICANT: KOH, Gou Young
 TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
 FILE REFERENCE: 10010-00001
 CURRENT APPLICATION NUMBER: US/10/273,180
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 2
 LENGTH: 260
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-273-180-2

Query Match 100.0%; Score 106; DB 4; Length 260;
 Best Local Similarity 100.0%; Pred. No. 2.5e-08; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

SEQ ID NO: 1 LCTKEGVLLKGKGKREBKEPF 20
 Db 1 LCTKEGVLLKGKGKREBKEPF 46

RESULT 5
 US-10-273-180-4
 Sequence 4, Application US/10273180
 Publication No. US20030220476A1
 GENERAL INFORMATION:
 APPLICANT: KOH, Gou Young
 TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
 FILE REFERENCE: 10010-00001

Query Match 100.0%; Score 106; DB 4; Length 312;
 Best Local Similarity 100.0%; Pred. No. 3e-08; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

SEQ ID NO: 1 LCTKEGVLLKGKGKREBKEPF 20
 Db 1 LCTKEGVLLKGKGKREBKEPF 97

RESULT 6
 US-10-273-180-6
 Sequence 6, Application US/10273180
 Publication No. US20030220476A1
 GENERAL INFORMATION:
 APPLICANT: KOH, Gou Young
 TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
 FILE REFERENCE: 10010-00001
 CURRENT APPLICATION NUMBER: US/10/273,180
 CURRENT FILING DATE: 2002-10-18
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 6
 LENGTH: 309
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-273-180-6

Query Match 100.0%; Score 106; DB 4; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3e-08; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

SEQ ID NO: 1 LCTKEGVLLKGKGKREBKEPF 20
 Db 75 LCTKEGVLLKGKGKREBKEPF 94

RESULT 7
 US-10-273-180-8
 Sequence 8, Application US/10273180
 Publication No. US20030220476A1
 GENERAL INFORMATION:
 APPLICANT: KOH, Gou Young
 TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
 FILE REFERENCE: 10010-00001
 CURRENT APPLICATION NUMBER: US/10/273,180
 CURRENT FILING DATE: 2002-10-18
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 8
 LENGTH: 312
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-273-180-8

Query Match 100.0%; Score 106; DB 4; Length 312;
 Best Local Similarity 100.0%; Pred. No. 3e-08; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

SEQ ID NO: 1 LCTKEGVLLKGKGKREBKEPF 20
 Db 78 LCTKEGVLLKGKGKREBKEPF 97

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RESULT 8
US-10-367-259A-36
; Sequence 36, Application US/10367259A
; GENERAL INFORMATION:
; APPLICANT: ELLIS, LEE M.
; TITLE OF INVENTION: ANGIOPOIETIN-1 IN THE TREATMENT OF DISEASE
; FILE REFERENCE: UTSC-698US
; CURRENT APPLICATION NUMBER: US/10/367,259A
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,809
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-259A-36

Query Match 100.0%; Score 106; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGKREBKEPF 20
Db 264 LCTKEGVLLKGKREBKEPF 283

RESULT 9
US-11-019-829-115
; Sequence 115, Application US/11019829
; Publication No. US20030136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: angiopoietin 1 variant 2
; LOCATION: (1) .. (402)
; OTHER INFORMATION: LocusID: 284; NM_139290
US-11-019-829-115

Query Match 100.0%; Score 106; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGKREBKEPF 20
Db 264 LCTKEGVLLKGKREBKEPF 283

RESULT 10
US-10-789-222-7
; Sequence 7, Application US/10789222
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10/789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,582
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-060-7

Query Match 100.0%; Score 106; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 4.e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGKREBKEPF 20
Db 222 LCTKEGVLLKGKREBKEPF 241

RESULT 11
US-10-789-222-8
; Sequence 8, Application US/10789222
; Publication No. US20040186054A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10/789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,582
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 8
; LENGTH: 456
; TYPE: PRT
; ORGANISM: mouse
US-10-789-222-8

Query Match 100.0%; Score 106; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 4.e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGKREBKEPF 20
Db 222 LCTKEGVLLKGKREBKEPF 241

RESULT 12
US-10-225-060-7
; Sequence 7, Application US/10225060
; Publication No. US20030093891A1
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-060-7

Query Match 100.0%; Score 106; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGKREBKEPF 20
Db 222 LCTKEGVLLKGKREBKEPF 241

```

Qy 1 LCTKEGVLLKGKGKREEEKKPF 20
 Db 244 LCTKEGVLLKGKGKREEEKKPF 263

RESULT 13
 US-10-928-911-7
 Sequence 7, Application US/10928911
 Publication No. US2005010699A1
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 Yancopoulos, George D.
 TITLE OF INVENTION: Expressed Ligand - Vascular
 Intercellular Signaling Molecule
 FILE REFERENCE: REG 333X
 CURRENT APPLICATION NUMBER: US/10/928,911
 PRIOR APPLICATION NUMBER: 10/245,060
 CURRENT FILING DATE: 2004-08-27
 PRIOR FILING DATE: 2002-08-21
 PRIOR APPLICATION NUMBER: 09/709,188
 PRIOR FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: 08/740,223
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 478
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-928-911-7

Query Match 100.0%; Score 106; DB 5; Length 478;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGKREEEKKPF 20
 Db 244 LCTKEGVLLKGKGKREEEKKPF 263

RESULT 14
 US-11-073-120-7
 Sequence 7, Application US/11073120
 Publication No. US2005018665A1
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 Yancopoulos, George D.
 TITLE OF INVENTION: Expressed Ligand - Vascular
 Intercellular Signaling Molecule
 FILE REFERENCE: REG 333X
 CURRENT APPLICATION NUMBER: US/11/073,120
 CURRENT FILING DATE: 2005-03-04
 PRIOR APPLICATION NUMBER: 10/225,060
 PRIOR FILING DATE: 2002-08-21
 PRIOR APPLICATION NUMBER: 09/709,188
 PRIOR FILING DATE: 2000-11-09
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 478
 TYPE: PRT
 ORGANISM: Homo sapien
 US-11-073-120-7

Query Match 100.0%; Score 106; DB 6; Length 478;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGKREEEKKPF 20
 Db 244 LCTKEGVLLKGKGKREEEKKPF 263


```

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-656-2598

Query Match 40.1%; Score 42.5%; DB 6; Length 163;
Best Local Similarity 47.6%; Pred. No. 4.1;
Matches 10; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

Qy 1 LCTKBEVILKLGK--GKREKEK 18
Db 142 ICPTEDKIAKGKVRGSREAPK 162

RESULT 5
US-10-467-657-7860
; Sequence 7860, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabeta
; TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7860
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7860

Query Match 38.7%; Score 41; DB 6; Length 134;
Best Local Similarity 72.7%; Pred. No. 5.5;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GVLKGGKREK 16
Db 16 GVLRGTKRED 26

RESULT 6
US-10-467-657-7966
; Sequence 7966, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabeta
; TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7966
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4826

Query Match 40.6%; Score 43; DB 6; Length 589;
Best Local Similarity 69.2%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GVLKGGKREK 18
Db 365 GVSLAGAKQSEBEK 377

RESULT 4
US-10-793-656-2598
; Sequence 2598, Application US/10793626
; Publication No. US2005255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMELLY, WILLIAM JOHN
; TITLE OF INVENTION: SPAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2598
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

Qy 6 GVLKKGKREB 16
 Db 276 GVLRLGTRKED 286

RESULT 7
 US-11-082-389-96
 ; Sequence 96, Application US/11082389
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kröger, Burkhard
 ; APPLICANT: Schröder, Hartwig
 ; APPLICANT: Zeidler, Oskar
 ; APPLICANT: Haberhauser, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT
 ; FILE REFERENCE: BGI-131CPN
 ; CURRENT APPLICATION NUMBER: US/11/082,389
 ; CURRENT FILING DATE: 2005-03-16
 ; PRIOR APPLICATION NUMBER: US/09/603024
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US/60/141031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US/60/143262
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: US/60/151281
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19930487.4
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19930489.0
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931549.3
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931550.7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19932134.5
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19941379.7
 ; PRIOR FILING DATE: 1999-08-31
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 446
 ; SEQ ID NO 96
 ; LENGTH: 412
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-11-082-389-96

Query Match 38.7%; Score 41; DB 7; Length 412;
 Best Local Similarity 70.0%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEGVILKGK 13
 Db 67 KDGVLKGKE 76

RESULT 8
 US-10-632-150-40
 ; Sequence 40, Application US/10632150
 ; Publication No. US20050251871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chiaur, D.
 ; APPLICANT: Pagan, M.
 ; APPLICANT: Latres, E.
 ; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
 ; FILE REFERENCE: 5914-081
 ; CURRENT FILING DATE: 2003-07-30
 ; PRIOR APPLICATION NUMBER: US/10/632,150
 ; PRIOR FILING DATE: 1999-08-27

Query Match 37.7%; Score 40; DB 6; Length 257;
 Best Local Similarity 46.7%; Pred. No. 17;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CTKEGVILKGKGRB 16
 Db 53 CQDBGLVPEGVGBEE 67

RESULT 9
 US-11-073-457-40
 ; Sequence 40, Application US/11073457
 ; Publication No. US2005026056A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagano, M.
 ; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
 ; FILE REFERENCE: 5914-050-999
 ; CURRENT APPLICATION NUMBER: US/11/073,457
 ; CURRENT FILING DATE: 2005-03-04
 ; PRIOR APPLICATION NUMBER: 10/042,417
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 60/260,179
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 40
 ; LENGTH: 257
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-073-457-40

Query Match 37.7%; Score 40; DB 7; Length 257;
 Best Local Similarity 46.7%; Pred. No. 17;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CTKEGVILKGKGRB 16
 Db 53 CQEQGLVPEGVGBEE 67

RESULT 10
 US-11-073-460-40
 ; Sequence 40, Application US/11073460
 ; Publication No. US20050272066A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagano, M.
 ; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
 ; FILE REFERENCE: 5914-090-999
 ; CURRENT APPLICATION NUMBER: US/11/073,460
 ; CURRENT FILING DATE: 2005-03-04
 ; PRIOR APPLICATION NUMBER: 10/042,417
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 60/260,179
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 40

LENGTH: 257
 TYPE: PRT
 ORGANISM: HOMO sapiens
 US-11-073-46-40

Query Match 37.7%; Score 40; DB 7; Length 257;
 Best Local Similarity 46.7%; Pred. No. 17;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGKREE 16
 Db 53 CQQBGLVPPGGVVE 67

RESULT 11

US-11-057-047-3

Sequence 3, Application US/11057047

Publication No. US20050260198A1

GENERAL INFORMATION:

APPLICANT: Holers, Vernon

APPLICANT: Thurman, Joshua

APPLICANT: Taube, Christian

APPLICANT: Gelfand, Erwin

APPLICANT: Gilkeson, Gary

TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and Methods Related Thereto

FILE REFERENCE: 2843-66

CURRENT APPLICATION NUMBER: US/11/057,047

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,594

PRIOR FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: 60/6316,239

PRIOR FILING DATE: 2004-12-14

PRIOR APPLICATION NUMBER: US04/015040

PRIOR FILING DATE: 2004-05-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.3

SEQ ID NO 3

LENGTH: 70

TYPE: PRT

ORGANISM: Homo sapiens

US-11-057-047-3

Query Match 36.8%; Score 39; DB 7; Length 70;
 Best Local Similarity 63.6%; Pred. No. 6.1;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKG 12
 Db 7 CSLEGVBKGG 17

RESULT 12

US-10-131-826A-280

Sequence 280, Application US/10131826A

Publication No. US20050245730A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tomas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William

Query Match 36.8%; Score 39; DB 7; Length 739;
 Best Local Similarity 43.8%; Prod. No. 23;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 KEGVLLKGKREE 19
 Db 175 KEGETIMKGHVKKXNP 190

RESULT 13

US-11-057-047-2

Sequence 2, Application US/11057047

Publication No. US20050260198A1

GENERAL INFORMATION:

APPLICANT: Holers, Vernon

APPLICANT: Thurman, Joshua

APPLICANT: Taube, Christian

APPLICANT: Gelfand, Erwin

APPLICANT: Gilkeson, Gary

TITLE OF INVENTION: The Alternative Complement Pathway and Methods Related Thereto

FILE REFERENCE: 2843-66

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,594

PRIOR FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: 60/6316,239

PRIOR FILING DATE: 2004-12-14

PRIOR APPLICATION NUMBER: US04/015040

PRIOR FILING DATE: 2004-05-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.3

SEQ ID NO 2

LENGTH: 739

TYPE: PRT

ORGANISM: Homo sapiens

US-11-057-047-2

Query Match 36.8%; Score 39; DB 7; Length 739;

Best Local Similarity 63.6%; Pred. No. 73; 2; Mismatches 2; Indels 0; Gaps 0; US-11-057-047-1

Query Match 36.8%; Score 39; DB 7; Length 764;

Best Local Similarity 63.6%; Pred. No. 76; 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12

Db 37 CSLEGEVIEKG 47

RESULT 14

US-11-057-047-6

Sequence 6, Application US/11057047

Publication No. US20050260198A1

GENERAL INFORMATION:

APPLICANT: Holers, Vernon

APPLICANT: Thurman, Joshua

APPLICANT: Taube, Christian

APPLICANT: Gelfand, Erwin

APPLICANT: Gilkeson, Gary

TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and Methods Related Thereto

FILE REFERENCE: 2848-66

CURRENT APPLICATION NUMBER: US/11/057,047

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,594

PRIOR FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: 60/636,239

PRIOR FILING DATE: 2004-12-14

PRIOR APPLICATION NUMBER: US04/015040

PRIOR FILING DATE: 2004-05-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.3

SEQ ID NO 6

LENGTH: 761

TYPE: PRT

ORGANISM: Mus musculus

US-11-057-047-6

RESULT 15

US-11-057-047-1

Sequence 1, Application US/11057047

Publication No. US20050260198A1

GENERAL INFORMATION:

APPLICANT: Holers, Vernon

APPLICANT: Thurman, Joshua

APPLICANT: Taube, Christian

APPLICANT: Gelfand, Erwin

APPLICANT: Gilkeson, Gary

TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and Methods Related Thereto

FILE REFERENCE: 2848-66

CURRENT APPLICATION NUMBER: US/11/057,047

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,594

PRIOR FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: 60/636,239

PRIOR FILING DATE: 2004-12-14

PRIOR APPLICATION NUMBER: US04/015040

PRIOR FILING DATE: 2004-05-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1

LENGTH: 764

TYPE: PRT

ORGANISM: Homo sapiens

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| |
|--|
| A:Experimental source: tadpole, brain |
| A:Note: this protein has motifs homologous to complement components C1r and C1s and to complement proteins C2 and C4. |
| C:Comment: This protein is a neuronal cell surface molecule involved in the neuronal recognition of self. |
| C:Superfamily: Xenopus A5 antigen, C1r/C1s repeat homology, discoidin I amino-terminal homology |
| C:Keywords: duplication, glycoprotein, transmembrane protein |
| F:1-21/Domain: signal sequence #status predicted <SIG> |
| F:22-92/Domain: A5 antigen #status predicted <MSA> |
| F:27-138/Domain: C1r/C1s repeat homology <CIR1> |
| F:147-362/Domain: C1r/C1s repeat homology <CIR2> |
| F:274-324/Domain: discoidin I amino-terminal homology <DN1> |
| F:430-564/Domain: discoidin I amino-terminal homology <DN2> |
| F:646-812/Domain: MAM homology <MAM> |
| F:861-883/Domain: transmembrane #status predicted <TM> |
| F:150-261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted |
| Query Match 44 3%; Score 47; DB 1; Length 927; |
| Best Local Similarity 53.3%; Pred. No. 44; |
| Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0; |
| Qy 6 GVLKGKGKREBKEPKP 20 |
| Db 498 GVIQGGKHKENKVP 512 |
| RESULT 8 |
| SYTHUTP |
| CTP synthase (EC 6.3.4.2) - human |
| N:Alternate names: CTP-synthetase; UTP-ammonia ligase |
| C:Species: Homo sapiens (man) |
| C:Accession: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 |
| R:Yamauchi, M.; Yamauchi, N.; Meuth, M. |
| EMBO J. 9, 2095-2099, 1990 |
| A:Title: Molecular cloning of the human CTP synthetase gene by functional complementation |
| A:Reference number: S12791; MUID:90291972; PMID:2113467 |
| A:Accession: S12791 |
| A: Molecule type: mRNA |
| A:Residues: 1-591 <YAM> |
| A:Cross-references: UNIPROT: P17812; UNIPARC:UPI0000163BFD; GB:X52142; NID:930292; PIDN:0095 |
| C:Comment: This enzyme is a glutamine amidotransferase that catalyzes the terminal reaction of the synthesis of CTP. |
| C:Keywords: ligase; pyrimidine nucleotide biosynthesis |
| Query Match 43 9%; Score 46.5; DB 1; Length 591; |
| Best Local Similarity 31.4%; Pred. No. 35; |
| Matches 11; Conservative 4; Mismatches 5; Indels 15; Gaps 1; |
| Qy 1 LCTKEGVLIKGG-----KREBKEPKP 20 |
| Db 361 LCSAHSGLVPGGFGVRGTEGKIQATAWNRQKPF 395 |
| RESULT 9 |
| S01371 |
| myosin heavy chain, cardiac and skeletal muscle - eastern newt (fragment) |
| C:Species: <i>Notophthalmus viridescens</i> , <i>Triturus viridescens</i> (eastern newt) |
| C:Date: 30-Sep-1998 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004 |
| C:Accession: S01371; S67907 |
| R:Casimir, C.M.; Gates, P.B.; Ross-Macdonald, P.B.; Jackson, J.F.; Patient, R.K.; Brocke, J. Mol. Biol. 202, 287-296, 1988 |
| A:Title: Structure and expression of a new cardio-skeletal myosin gene. Implications for the evolution of myosin genes. |
| A:Reference number: S01371; MUID:9011937; PMID:2459393 |
| A:Status: not compared with conceptual translation |
| A:Molecule type: DNA |
| A:Residues: 1-171 <CAS> |
| A:Cross-references: UNIPROT: Q7LZ84; UNIPARC:UPI0000177608 |
| A:Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 64-1le. |
| A:Accession: S67907 |

RESULT 13
 T29766
 hypothetical protein ZC581.5 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Accession: T29766
 C;Description: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 R;Waterston, B.; Gattung, S.; Le, T.T.
 Submitted to the EMBL Data Library, May 1997
 A;Reference number: Z20582
 A;Accession: T29766
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-197 <WAT>
 A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AP003134; PIDN:AAB54143.1; GSPDB:GN00019
 A;Experimental source: strain Bristol N2; clone ZC581
 C;Genetics:
 A;Gene: CESP:ZC581.5
 A;Map position: 1
 A;Introns: 74/1

Query Match 41.5%; Score 44; DB 2; Length 97;
 Best Local Similarity 53.8%; Pred. No. 15;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 EGVLJKGKREBEE 17
 DB 31 ERIMMKGGKNEBD 43

RESULT 14
 T48751
 hypothetical protein 8D4.250 [Imported] - *Neurospora crassa*
 C;Species: *Neurospora crassa*
 C;Accession: T48751
 C;Description: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,
 Submitted to the Protein Sequence Database, April 2000
 A;Reference number: Z24541
 A;Accession: T48751
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-141 <SCH>
 A;Cross-references: UNIPARC:UPI0000179478; EMBL:AL353819; GSPDB:GN00112; NCSP:8D4.250
 C;Genetics:
 A;Gene: NCSP:8D4.250
 A;Map position: 2

RESULT 15
 T20508
 hypothetical protein F02E9.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Accession: T20508
 C;Description: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R;Gray, I.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19285
 A;Accession: T20508
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-154 <WIL>
 A;Cross-references: UNIPROT:O01314; UNIPARC:UPI0000074F98; EMBL:Z81494; PIDN:CA04047.1;
 C;Genetics:
 A;Gene: CESP:F02E9.1
 A;Map position: 1
 A;Introns: 29/2; 52/2; 80/3; 131/3

Query Match 41.5%; Score 44; DB 2; Length 154;
 Best Local Similarity 60.0%; Pred. No. 23;
 Matches 12; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 LCTKKG-*V*LTKGGKREBEE 18
 DB 53 LDTKNGKFVLLKNSBNBEEK 72

Search completed: December 29, 2005, 15:40:56
 Job time : 38 secs

C;Superfamily: Neurospora crassa hypothetical protein 8D4.250
 C;Species: *Neurospora crassa*
 C;Accession: S15675
 C;Description: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 R;Wallace, N.H.; Krii, A.L.
 Plant Physiol. 95, 973-975, 1991
 A;Title: Nucleotide sequence of a cDNA clone corresponding to the maize globulin-2 gene.
 A;Reference number: S15675
 A;Accession: S15675
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-450 <WAL>
 A;Cross-references: UNIPROT:Q7ML1Z8; UNIPARC:UPI0000177E41
 C;Superfamily: vicilin
 C;Species: *Neurospora crassa*
 C;Accession: T20508
 C;Description: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R;Gray, I.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19285
 A;Accession: T20508
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-154 <WIL>
 A;Cross-references: UNIPROT:O01314; UNIPARC:UPI0000074F98; EMBL:Z81494; PIDN:CA04047.1;

| | | | | | | | |
|--|--|-------|--------|--------|--------|---------|---------------------------------|
| Scoring table: | BLOSUM62 | | | | | | |
| Gapop: | 10.0 , Gapext: 0.5 | | | | | | |
| Searched: | 2166443 seqs, 705528306 residues | | | | | | |
| Total number of hits satisfying chosen parameters: | 2166443 | | | | | | |
| Minimum DB seq length: | 0 | | | | | | |
| Maximum DB seq length: | 2000000000 | | | | | | |
| Post-processing: | Minimum Match 0\$ Maximum Match 100\$ Listing first 45 summaries | | | | | | |
| Database : | Uniprot_05..80:* | | | | | | |
| | 1: uniprot_sprot:* | | | | | | |
| | 2: uniprot_trembl:* | | | | | | |
| Pred. No. | is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | |
| SUMMARIES | | | | | | | |
| Result No. | Score | Query | Match | Length | DB | ID | Description |
| 1 | 106 | 100.0 | Q5Y1W1 | 2 | Q5Y1W1 | HUMAN | Q5Y1W1 homo sapien |
| 2 | 106 | 100.0 | Q5Y1W1 | 1 | ANGP1 | HUMAN | Q15389 homo sapien |
| 3 | 106 | 100.0 | Q5Y1W1 | 1 | ANGP1 | MOUSE | Q08338 mus musculus |
| 4 | 106 | 100.0 | Q5Y1W1 | 2 | Q5Y1W1 | HUMAN | Q5Y1W1 homo sapien |
| 5 | 106 | 100.0 | Q5Y1W1 | 2 | Q5Y1W1 | MOUSE | Q6mv77 mus musculus |
| 6 | 106 | 100.0 | Q5Y1W1 | 2 | Q8C2K6 | MOUSE | Q8C2K6 mus musculus |
| 7 | 96 | 90.6 | Q5Y1W1 | 2 | Q9BDY8 | PIG | Q9BDY8 sus scrofa |
| 8 | 89.5 | 84.4 | Q5Y1W1 | 1 | Q8N6P1 | HUMAN | Q8n6p3 homo sapien |
| 9 | 89.5 | 84.4 | Q5Y1W1 | 1 | ANGP1 | RAT | Q35460 rattus norvegicus |
| 10 | 89.5 | 84.4 | Q5Y1W1 | 2 | Q6A0F0 | MOUSE | Q6a0f0 mus musculus |
| 11 | 86.5 | 81.6 | Q5Y1W1 | 2 | Q6OFC1 | CANINE | Q6ofc1 canis familiaris |
| 12 | 85.5 | 80.7 | Q5Y1W1 | 1 | ANGP1 | BOVINE | Q18220 bos taurus |
| 13 | 76 | 71.7 | Q5Y1W1 | 2 | Q6GNY4 | XENIA | Q6gny4 xenopus laevis |
| 14 | 59 | 55.7 | Q5Y1W1 | 2 | Q9CUL6 | MOUSE | Q9cul6 mus musculus |
| 15 | 55 | 51.9 | Q5Y1W1 | 1 | Q4RNQ8 | TEETING | Q4rnq8 tetractodon nigroviridis |
| 16 | 54 | 50.9 | Q5Y1W1 | 2 | Q8H7M2 | ORVISA | Q8h7m2 oryza sativa |
| 17 | 53 | 50.0 | Q5Y1W1 | 2 | Q8BA48 | FEFLAV | Q8ba48 iguape viridis |
| 18 | 52.5 | 49.5 | Q5Y1W1 | 2 | Q5XHAB | XENIA | Q5xhab xenopus laevis |
| 19 | 51 | 48.1 | Q5Y1W1 | 2 | Q8I6U1 | CIOSEA | Q8i6u1 ciona savignyi |
| 20 | 51 | 48.1 | Q5Y1W1 | 2 | Q9CST2 | MOUSE | Q9cst2 mus musculus |
| 21 | 51 | 48.1 | Q5Y1W1 | 2 | Q7Y188 | ORVISA | Q7y188 oryza sativa |
| 22 | 51 | 48.1 | Q5Y1W1 | 2 | Q7Y017 | ORVISA | Q7y017 oryza sativa |
| 23 | 51 | 48.1 | Q5Y1W1 | 2 | Q7XDX7 | ORVISA | Q7xdx7 oryza sativa |
| 24 | 51 | 48.1 | Q5Y1W1 | 2 | Q6L423 | ORVISA | Q6l423 oryza sativa |
| 25 | 51 | 48.1 | Q5Y1W1 | 2 | Q7XWN4 | ORVISA | Q7xwn4 oryza sativa |
| 26 | 51 | 48.1 | Q5Y1W1 | 2 | Q6K055 | ORVISA | Q6k055 oryza sativa |
| 27 | 51 | 48.1 | Q5Y1W1 | 2 | Q5KQ96 | ORVISA | Q5kq96 oryza sativa |
| 28 | 51 | 48.1 | Q5Y1W1 | 2 | Q75J33 | ORVISA | Q75j33 oryza sativa |
| 29 | 51 | 48.1 | Q5Y1W1 | 2 | Q75HCL | ORVISA | Q75hcl oryza sativa |
| 30 | 51 | 48.1 | Q5Y1W1 | 2 | Q6L559 | ORVISA | Q6l559 oryza sativa |
| 31 | 51 | 48.1 | Q5Y1W1 | 2 | Q94GS7 | ORVISA | Q94gs7 oryza sativa |

SEQUENCE REVISION. MEDLINE=2215863; PubMed=12168954;
Kikuno R., Ohara O., Nagase T., Yamakawa H., Otsukai N., Kajimura D., Construction of expression-ready cDNA clones for KIAA genes: manual cloning of 330 KIAA cDNA clones.; DNA Res. 9:99-106 (2002).

1- FUNCTION: Binds and activates TIE2 receptor by inducing its tyrosine phosphorylation. Implicated in endothelial developmental processes later and distinct from that of VEGF. Appears to play a crucial role in mediating reciprocal interactions between the endothelial and surrounding matrix and mesenchyme. Mediates blood vessel maturation/stabilization. It may play an important role in the vessel maturation/stabilization.

- heart early development.
- SUBCELLULAR LOCATION: Secreted.
- PTM: GLYCOSYLATED.
- MISCELLANEOUS: It may have a potential therapeutic utility since it can be used for specifically targeting tumor vasculature or for promoting angiogenic processes in certain organs such as an ischemic heart.
- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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PROSTATE: PS00514; FIBRIN: 1. AG C DOMAIN; 1. Fibrinogen; Coiled coil; Developmental protein; Differentiation; Fibrinogen; Signal. BILLYCOPROTEIN: Polymorphism; Signal. SIGNAL: 15 SIGNAL: 16 Angiopoietin-1. CHAIN: 16 498 Angiopoietin-1.

| ANGPT1_MOUSE | ID | ANGPT1_MOUSE | STANDARD | PRT; | 498 AA. |
|--------------|---|-----------------------------------|----------|------|---------|
| AC | 008538; | | | | |
| DT | 16-OCT-2001 | (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 | (Rel. 40, Last sequence update) | | | |
| DT | 10-MAY-2005 | (Rel. 47, Last annotation update) | | | |
| DE | Angiopoietin-1 precursor (ANG-1). | | | | |
| GN | Name=Angpt1; Synonyms=Angpt; | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; | | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; | | | | |
| OC | Muroidea; Muridae; Murinae; Mus. | | | | |
| OC | NCBI TaxID:10090; | | | | |

[1] NUCLEOTIDE SEQUENCE.
RN MEDLINE=97134663; PubMed=8980223; DOI=10.1016/S0092-
RP RX
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton A.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisonneuve
RA Vancopoulos G.D.,
RA "Isolation of angiopoietin-1, a ligand for the Tie2 receptor."
RT RT
RT secretion-trap expression cloning;"

Cell 87:1167-1169 (1996).
 RL -1- FUNCTION: Binds and activates TIE2 receptor by tyrosine phosphorylation. Implicated in endothelial processes later and distinct from that of VEGF. crucial role in mediating reciprocal interaction between endothelial and surrounding matrix and mesenchymal cells during angiogenesis. TIE2 may play an important role in vascular maturation and stability.

- heart early development.
- SUBCELLULAR LOCATION: Secreted.
- DEVELOPMENTAL STAGE: Early in development, at E14.5 found most prominently in the heart myocardium and endocardium. Later, it becomes more widely distributed in the mesenchyme surrounding developing vessels in association with endothelial cells.
- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

This Swiss-Prot entry is copyright. It is produced

DR GO:0005172; P:vascular endothelial growth factor receptor. . . ; TAS.
 GO: GO:0007422; P:endothelium development; TAS.
 GO: GO:0007159; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
 InterPro: IP0002101; Fibrinogen_C.
 DR Pfam: PF00147; Fibrinogen_C_1.
 SMART: SM00186; FG1; 1.
 PROSITE: PS00514; FIBRIN AG C DOMAIN; 1.
 KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
 KW Glycoprotein; Signal.

FT Potential.. 1 19
 SIGNAL 19
 FT CHAIN 20 498 Angiopoietin-1.
 FT DOMAIN 284 498 Fibrinogen C-terminal.
 FT COILED 81 119 Potential..
 FT COILED 153 261 Potential.. (GlcNAc. . .) (Potential).
 FT CARBOHYD 92 92 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 122 122 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 154 154 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 243 243 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 295 295 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 286 315 By similarity.
 FT DISULFID 439 452 By similarity.
 FT SEQUENCE 498 AA; 57505 MN; 285B4FB26D800 CRC64;
 Query Match 100.0%; Score 106; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRREEEKPP 20
 Db 264 LCTKEGVLLKGKGRREEEKPP 283

RESULT 4
 Q5HYAO HUMAN
 ID Q5HYAO_HUMAN PRELIMINARY; PRT; 498 AA.
 AC Q5HYAO_1
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Hypothetical protein DKRZP68510222.
 GN Name=DKRZP68510222;
 Homo sapiens (Human);
 Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 Homo.
 NCBI_TaxID=9606;

RN NUCLEOTIDE SEQUENCE;
 TISSUE=small intestine;
 RG The German cDNA Consortium;
 RA Bahr A., Lauber J., Meves H.W., Weil B., Amid C., Obanger A., Pobo G.,
 RA Han M., Wiemann S.,
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; B648814; CAT45984.1; -; mRNA.
 KW Hypothetical protein.

SEQUENCE 498 AA; 57513 MN; 5D5FA63AEF6BE920 CRC64;

Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRREEEKPP 20
 Db 264 LCTKEGVLLKGKGRREEEKPP 283

RESULT 5
 Q6NWV7 MOUSE
 ID Q6NWV7_MOUSE PRELIMINARY; PRT; 498 AA.
 AC Q6NWV7_1
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Angiopoietin 1.
 Name=Angpt1;
 Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Embryo; DOI=10.1073/pnas.242603899;
 RX MEDLINE:22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheetz T.E.,
 RA Hopkins R.P., Jordan J., Moore T., Max S.I., Wang J., Haiech P.,
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Steapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Yoshiyuki S., Crimminci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnaratin P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
 RA Rodriguez A.C., Touchman J.W., Dickson M.C.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,
 RA Schenrich A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]

RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Embryo;
 RC Director MGC Project;
 RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC067410; AAH67410.1; -; mRNA.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005172; P:vascular endothelial growth factor receptor. . . ; TAS.
 DR GO; GO:0007492; P:endothelial growth factor receptor. . . ; TAS.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
 DR InterPro; IPR02181; Fibrinogen_C.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN AG_C_DOMAIN; 1.
 DR SEQUENCE 498 AA; 57513 MN; FC36F05A9E79074 CRC64;

Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRREEEKPP 20
 Db 264 LCTKEGVLLKGKGRREEEKPP 283

RESULT 6
 Q8C2K6 MOUSE
 ID Q8C2K6_MOUSE PRELIMINARY;
 AC Q8C2K6_1
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus 2 days neonate thymus cDNA, RIKEN full-length enriched library, clone: B43 0016L03 product: angiopoietin, full DE insert sequence.
 DE Name=Angpt1;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]

| | |
|---|--|
| RP | NUCLEOTIDE SEQUENCE. |
| RC | STRAIN=NO; TISSUE=Thymus; |
| RX | MEDLINE=9927253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; |
| RA | Carninci P.; Hayashizaki Y.; |
| RT | "High-efficiency full-length cDNA cloning."; |
| RL | Math. Enzymol. 303:19-44(1999). |
| RN | [2] |
| NUCLEOTIDE SEQUENCE. | |
| RC | STRAIN=NO; TISSUE=Thymus; |
| RX | MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500; |
| RA | Kawai J., Shinagawa A., Shitara K., Yoshino M., Itoh M., Ishii Y., |
| RA | Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., |
| RA | Aizawa K., Iwasa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., |
| RA | Saito T., Okazaki K., Gojobori T., Bono H., Kasukawa T., Saito R., |
| RA | Katoh K., Matsuda H., Aishburner M., Baralov S., Carninci P., |
| RA | Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., |
| RA | Kuehl P., Lewis S., Matsuo F., Nikaido I., Pesole G., Quadeckbush J., |
| RA | Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., |
| RA | Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., |
| RA | Blake J., Boffelli D., Bojunga J., Carninci P., de Bonaldo M.P., |
| RA | Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., |
| RA | Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., |
| RA | Lyons P., Marchionni L., Mazzarelli J., Mazzarelli P., Mombartts P., |
| RA | Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., |
| RA | Sasaki H., Sato K., Schoenbach C., Seya T., Shitara Y., Storch K.-F., |
| RA | Suzuki H., Toyo-oka K., Wang K.H., Wetz C., Whittaker C., Wilming L., |
| RA | Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlbuski S., |
| RA | Hayashizaki Y.; |
| RT | "Functional annotation of a full-length mouse cDNA collection."; |
| RL | Nature 409:685-690(2001). |
| RN | [3] |
| RP | NUCLEOTIDE SEQUENCE. |
| RC | The PANTOM Consortium, |
| RT | the RIKEN Genome Exploration Research Group Phase I & II Team; |
| RT | "Analysis of the mouse transcriptome based on functional annotation of |
| RT | 60,770 full-length cDNAs."; |
| RN | Nature 420:563-573 (2002). |
| [4] | NUCLEOTIDE SEQUENCE. |
| STRAIN=NO; TISSUE=Thymus; | |
| RA | Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P., |
| RA | Medline=20499374; PubMed=11042159; DOI=10.1101/gr.145100; |
| RA | Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shitara K., Itoh M., |
| RA | Konno H., Okazaki K., Muramatsu M., Hayashizaki Y.; |
| RT | "Normalization and subtraction of cap-trapper-selected cDNAs to |
| RT | prepare full-length cDNA libraries for rapid discovery of new genes."; |
| RL | Genome Res. 10:1617-1630 (2000). |
| RN | [5] |
| RP | NUCLEOTIDE SEQUENCE. |
| STRAIN=NO; TISSUE=Thymus; | |
| RA | Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P., |
| RA | Medline=20530913; PubMed=11076861; DOI=10.1101/07.152600; |
| RA | Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., |
| RA | Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., |
| RA | Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., |
| RA | Fujikawa S., Inoue K., Togawa Y., Iwasa M., Ohara E., Watahiki M., |
| RA | Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J., |
| RA | Okazaki Y., Muramatsu M., Inoue Y., Kiria A., Hayashizaki Y., |
| RT | "RIKEN integrated sequence analysis (RISA) system-384-format |
| RT | sequencing Pipeline with 384 multicapillary sequencer."; |
| RL | Genome Res. 10:1757-1771 (2000). |
| [6] | NUCLEOTIDE SEQUENCE. |
| RC | STRAIN=NO; TISSUE=Thymus; |
| RA | Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., |
| RA | Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., |
| RA | Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T., |
| RA | Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Katukawa T., |
| RA | Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., |
| RA | Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., |
| RA | Nishi K., Nomura K., Numazaki R., Ohno M., Ohzato N., Sano H., |
| RA | Saito R., Saitoh H., Sakai C., Sakai K., Sakurai T., Sogabe Y., Tagami M., |
| RA | Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., |
| RA | Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T., |
| RA | Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; |
| RL | Submitted (APR-2002) to the EMBL/GenBank/DBJ databases. |
| DR | EMBL; AK088439; BAC40354.1; -; mRNA. |
| DR | HSSP; P02671; 1PZD. |
| DR | MG1: MG1:108448; Angpt1. |
| DR | InterPro; IPR02181; Fibrinogen_C. |
| DR | Pfam; PF00147; Fibrinogen_C. |
| DR | SMART; SM00186; FBRG; 1. |
| DR | PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. |
| DR | SEQUENCE 498 AA; 5745 MW; 285D97468CSD800 CRC64; |
| Query Match | 100.0%; Score 106; DB 2; Length 498; |
| Best Local Similarity | 100.0%; Pred. 0.1.8e-07; |
| Matches | 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 LCYKEGVLLKGGRREBKEPF 20 |
| Do | 264 LCYKEGVLLKGGRREBKEPF 283 |
| RESULT 7 | |
| Q9BDY8_PIG | PRELIMINARY; |
| ID Q9BDY8_PIG | PRT; 498 AA. |
| AC Q9BDY8_PIG | |
| Q9BDY8_PIG | 17, Created) |
| AC Q9BDY8_PIG | 01-JUN-2001 (TREMBLrel. 17, Last sequence update) |
| AC Q9BDY8_PIG | 01-MAR-2004 (TREMBLrel. 26, Last annotation update) |
| DB | DB |
| OS Sus scrofa (Pig). | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae; Sus scrofa; (Pig). | |
| OC Mammalia; Eutheria; Laurasiatheria; Laurasiatheria; Suidae; Sus scrofa; (Pig). | |
| OC NCBTAXID=9823; | |
| OX [1] | |
| RN | NUCLEOTIDE SEQUENCE. |
| RP | MEDLINE=21151163; PubMed=11230987; DOI=10.1016/S0008-6363(00)00295-9; |
| RX | "The angiopoietin2 system in coronary artery endothelium prevents |
| RT | oxidized low-density lipoprotein-induced apoptosis."; |
| RL | Cardiovasc. Res. 49:872-881 (2001). |
| DR | EMBL; AF233227; AAC14932.1; -; mRNA. |
| DR | HSSP; P02671; 1PZD. |
| DR | InterPro; IPR02181; Fibrinogen_C. |
| DR | Pfam; SM00186; FBRG; 1. |
| DR | SMART; SM00186; FBRG; 1. |
| DR | PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. |
| SQ | SEQUENCE 498 AA; 57413 MW; ABC1C8BF56061876 CRC64; |
| Query Match | 90.6%; Score 96; DB 2; Length 498; |
| Best Local Similarity | 90.0%; Pred. No. 6e-06; |
| Matches | 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0; |
| Qy | 1 LCYKEGVLLKGGRREBKEPF 20 |
| Do | 264 LCYKEGVLLKGGRREBKEPF 283 |
| RESULT 8 | |
| Q8NQP3_HUMAN | PRELIMINARY; |
| ID Q8NQP3_HUMAN | PRT; 147 AA. |
| AC Q8NQP3 | |
| Q8NQP3_HUMAN | 22, Created) |
| ID Q8NQP3 | 01-OCT-2002 (TREMBLrel. 22, Last sequence update) |
| AC Q8NQP3 | 01-OCT-2003 (TREMBLrel. 23, Last sequence update) |
| DR | ANGPTL Proteins. |
| OS Homo sapiens (Human) | |
| OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Cetartiodactyla; Eutheria; Laurasiatheria; Laurasiatheria; Suidae; Sus scrofa; (Human) | |
| OC NCBTAXID=9666; | |
| RN | [1] |

| | |
|-----------------------|--|
| RP | NUCLEOTIDE SEQUENCE. |
| RC | TISSUE=Prostate; PubMed=12477932; DOI=10.1073/pnas.242601899; |
| RX | Strausberg R.L., Feilngold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collman P.S., Wagner L.H., Schaeffer C.M., Schuler G.D., Altchul S.F., Zeeberg B., Buetow K.H., Shenafer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marsuska K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Cabavant T.L., Scheetz T.E., Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquai Lano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heitton B., Kerttman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.-B., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). |
| RN | [2] |
| RP | NUCLEOTIDE SEQUENCE. |
| RA | Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. |
| RL | EMBL: BC029406; AAC29406.1; -; mRNA. |
| DR | HSSP; P04671; 1FZD. |
| DR | InterPro: IPR002181; Fibrinogen_C; 1. |
| DR | Pfam: PF00147; Fibrinogen_C. |
| DR | PROSITE: PS00514; FIBRIN AG C DOMAIN; 1. |
| DR | SMART: SM00186; FBG; 1. |
| DR | SMART: SM00186; FBG; 1. |
| DR | Pfam: PF00147; Fibrinogen_C; 1. |
| DR | SMART: SM00186; FBG; 1. |
| SQ | SEQUENCE 147 AA; 17314 MW; 68DRD40DB06FA37E CRC64; |
| Query Match | Score 89.5; DB 2; Length 147; |
| Best Local Similarity | 94.4%; Pred. No. 1.8e-05; |
| Matches | 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1; |
| Qv. | 1 LCTKEGVLLKGKGRBEEKPF 20 |
| Db | 10 LCTKE-VLLKGKGRBEEKPF 28 |
| RESULT 9 | |
| ID | ANGP1_RAT STANDARD; PRT; 497 AA. |
| AC | Q35160; Q8K4Q1; |
| DT | 16-OCT-2001 (Rel. 40, Created) |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) |
| DT | 10-MAY-2005 (Rel. 47, Last annotation update) |
| DB | Angiopoietin-1 precursor (ANG-1). |
| GN | Name=Angpt1; |
| OS | Rattus norvegicus (Rat). |
| OC | Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Muroidea; Muridae; Murinae; Rattus. |
| NCBI_TaxID | 10116; |
| RN | [1] |
| RP | NUCLEOTIDE SEQUENCE. |
| RC | STRAIN=Nistar; TISSUE=Placenta; MEDLINE=42346196; PubMed=12458684; DOI=10.1023/A:1020921818105; |
| RA | Iizasa H., Bae S.H., Asashima T., Kitano T., Matsunaga N., Terasaki T., Kang Y.S., Nakashima E., |
| RT | "Augmented expression of the tight junction protein occludin in brain endothelial cell line TR-BBB by rat angiopoietin-1 expressed in baculovirus-infected sf plus insect cells." |
| RL | Pharm. Res. 19:1757-1760 (2002). |
| RN | [2] |
| RP | NUCLEOTIDE SEQUENCE OF 91-200. |
| RC | STRAIN=Sprague-Dawley; TISSUE=Placenta; |
| RX | MEDLINE=8451564; PubMed=9776732; |
| RA | Mandriota S.J., Pepper M.S.; |
| NCBI_TaxID | 10090; |
| RT | "Regulation of angiopoietin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia." |
| RL | Circ. Res. 83:852-859 (1998). |
| CC | -i- FUNCTION: Binds and activates TIE2 receptor by inducing its tyrosine phosphorylation. Implicated in endothelial developmental processes later and distinct from that of VEGF. Appears to play a crucial role in mediating reciprocal interactions between the endothelium and surrounding matrix and mesenchyme. Mediates blood vessel maturation/stability. It may play an important role in the heart early development. |
| CC | -i- SIMILARITY: Contains 1 Fibrinogen C-terminal domain. |
| CC | This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. |
| CC | DR EMBL: AB08023; BAC10290.1; -; mRNA. |
| DR | EMBL: AF030376; AAC78246.1; -; mRNA. |
| DR | HSSP; P02671; 1FZD. |
| DR | Ensembl: ENSRNOG0000005854; Rattus norvegicus. |
| DR | RGD; 628896; Angpt1. |
| DR | GO: 0005102; P: receptor binding; TAS. |
| DR | GO: 0001525; P: angiogenesis; IEP. |
| DR | GO: 004014; P: Tie receptor signaling pathway; IDA. |
| DR | InterPro: IPR002181; Fibrinogen_C. |
| DR | PFAM: PF00147; Fibrinogen_C; 1. |
| DR | SMART: SM00186; FBG; 1. |
| DR | PROSITE: PS00514; FIBRIN AG C DOMAIN; 1. |
| KW | Angiogenesis; Coiled coil; Developmental protein; Differentiation; Glycoprotein; Signal. |
| KW | Potential. |
| FT | SEQUENCE 1 19 |
| FT | Angiopoietin-1. |
| FT | CHAIN 20 497 |
| FT | Fibrinogen C-terminal. |
| FT | Potential. |
| FT | COILED 283 497 |
| FT | Potential. |
| FT | CARBOHYD 81 119 |
| FT | Potential. |
| FT | CARBOHYD 153 261 |
| FT | Potential. |
| FT | N-Linked (GlcNAc. . .) (Potential). |
| FT | CARBOHYD 92 92 |
| FT | Potential. |
| FT | N-Linked (GlcNAc. . .) (Potential). |
| FT | CARBOHYD 122 122 |
| FT | Potential. |
| FT | CARBOHYD 154 154 |
| FT | Potential. |
| FT | N-Linked (GlcNAc. . .) (Potential). |
| FT | CARBOHYD 243 243 |
| FT | Potential. |
| FT | N-Linked (GlcNAc. . .) (Potential). |
| FT | CARBOHYD 294 294 |
| FT | Potential. |
| FT | N-Linked (GlcNAc. . .) (Potential). |
| FT | DISULFID 285 314 |
| FT | By similarity. |
| FT | DISULFID 438 451 |
| FT | By similarity. |
| FT | CONFLICT 98 98 |
| FT | Q > E (in Ref. 2). |
| FT | CONFLICT 172 172 |
| FT | E > K (in Ref. 2). |
| FT | CONFLICT 189 189 |
| FT | E > K (in Ref. 2). |
| SEQUENCE | 497 AA; 57461 MW; 08E66ABEFD68AB CRC64; |
| Query Match | 84.4%; Score 89.5; DB 1; Length 497; |
| Best Local Similarity | 95.0%; Pred. No. 6e-05; |
| Matches | 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1; |
| Qv. | 1 LCTKEGVLLKGKGRBEEKPF 20 |
| Db | 10 LCTKE-VLLKGKGRBEEKPF 28 |
| RESULT 10 | |
| Q6A0F0_MOUSE | NUCLEOTIDE SEQUENCE. |
| ID | Q6A0F0_MOUSE PRELIMINARY; |
| AC | Q6A0F0; |
| DT | 25-OCT-2004 (TREMBLrel. |
| DT | 25-OCT-2004 (TREMBLrel. |
| DT | 25-OCT-2004 (TREMBLrel. |
| DE | MKIQA0003 protein (Fragment). |
| GN | Name=Angpt1; Synonyms=mKIQA0003; |
| OS | Mus musculus (Mouse). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; |
| OC | Mammalia; Eutheria; Buiarchontoglires; Glires; Rodentia; Murinae; Muridae; Murinae; Mus. |
| OC | Muridae; Murinae; Mus. |
| OX | NCBI_TaxID=10090; |

| | | | |
|------------------------------|--|----------|--|
| AC | 01820; | DT | 16-OCT-2001 (Rel. 40, Created) |
| RP | NUCLEOTIDE SEQUENCE. | DT | 16-OCT-2001 (Rel. 40, Last sequence update) |
| RC | TISSUE-Adult spleen; | DT | 10-MAY-2005 (Rel. 47, Last annotation update) |
| RX | PubMed:1536895; | DB | Angiopoletin-1 Precursor (ANG-1) (Fragment). |
| RA | Okazaki N.; Kikuno R.; Ohara R.; Inamoto S.; Koseki H.; Hiraoka S.; | GN | Name=ANGF1; Synonyms=ANG1; |
| RA | Saga Y.; Seino S.; Niimura M.; Kaihoh T.; Hoshino K.; Kitamura H., | OS | Bos taurus (Bovine). |
| RA | Nagase T.; Ohara O.; Koga H.; | OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| RT | "Prediction of the coding sequences of mouse homologues of KIAA gene: | OC | Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; |
| IV | IV." The complete nucleotide sequences of 500 mouse KIAA homologous | OC | Pecora; Bovidae; Bovinae; Bos. |
| RT | cdNAAs identified by screening of terminal sequences of cDNA clones | OX | NCBI_TaxID:9913; |
| RT | randomly sampled from size-fractionated libraries."; | RN | [1] |
| DN | DNA Res. 11:205-218(2004). | RP | NUCLEOTIDE SEQUENCE. |
| RL | EMBL; AK12868; BAD32146.1; -; mRNA. | RC | TISSUE=Ovary; |
| DR | MGI; MGI:1084448; Ansg01. | RX | Medline=99054348; PubMed=9840613; |
| DR | GO; GO:0005615; C:extracellular space; TAS. | RA | Goedde V.; Schmidt T.; Kimmela S.; Kozian D.; Augustin H.G.; |
| DR | GO; GO:0005172; C:vascular endothelial growth factor receptor. . .; TAS. | RT | "Analysis of blood vessel maturation processes during cyclic ovarian angiogenesis."; |
| DR | GO; GO:0007492; P:endothelial development; TAS. | RT | "Analysis of blood vessel maturation processes during cyclic ovarian angiogenesis."; |
| DR | GO; GO:000169; P:transmembrane receptor protein tyrosine kin. . .; IDA. | RL | Lab. Invest. 78:1385-1394(1998). |
| DR | InterPro; IPR0181; Fibrinogen_C. | RN | [2] |
| PFam | PF00147; Fibrinogen_C; 1. | RP | NUCLEOTIDE SEQUENCE OF 91-200 |
| DR | SMART; SM00186; 1. | RC | TISSUE=Liver; |
| DR | PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. | RX | Medline=8451564; PubMed=9776732; |
| FT | NON_TER 1 1 | RA | Mandriota S.J.; Pepper M.S.; |
| SEQUENCE | 521 AA; 60103 MW; 8E7061F2A570EDFA CRC64; | RT | "Regulation of angiopoietin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia." |
| SQ | . | RT | Regulation of angiopoietin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia." |
| Query Match | Score 89.5; DB 2; Length 521; | RL | Circ. Res. 83:852-859(1998) |
| Best Local Similarity | 95.0%; Pred. No. 6.2e-05; | CC | -!- FUNCTION: Binds and activates TIE2 receptor by inducing its tyrosine phosphorylation. Implicated in endothelial developmental processes later and distinct from that of VEGF. Appears to play a crucial role in mediating reciprocal interactions between the endothelium and surrounding matrix and mesenchyme. Mediates blood vessel maturation/stability. It may play an important role in the heart early development (By similarity). |
| Matches 19; | Conservative 0; Mismatches 0; Indels 1; Gaps 1; | CC | -!- SUBCELLULAR LOCATION: Secreted. |
| Qy | 1 LCTKREGVLLKGKREEEKPF 20 | CC | -!- DEVELOPMENTAL STAGE: Found to be expressed throughout the ovarian cycle. |
| Db | 286 LCTKE-VLLKGKREEEKPF 306 | CC | -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain. |
| RESULT 11 | | CC | This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is removed. |
| ID | Q60FC1_CANFA PRELIMINARY; | PRT; | 497 AA. |
| Q60FC1; | | | |
| AC | | | |
| DT | 25-OCT-2004 (TREMBLrel. 28; Last sequence update) | | |
| DT | 25-OCT-2004 (TREMBLrel. 28; Last annotation update) | | |
| DT | 25-OCT-2004 (TREMBLrel. 28; Last annotation update) | | |
| DB | Angiopoletin-1. | | |
| GN | Name=Ang-1; | | |
| OS | Canis familiaris (Dog). | | |
| OC | Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; | | |
| OC | Canis | | |
| NCBI_TAXID=9615; | | | |
| OX | | | |
| RN | [1] | | |
| RP | NUCLEOTIDE SEQUENCE. | | |
| RA | Kato Y.; Asano K.; | | |
| RT | "Canis familiaris Angiopoletin-1 mRNA, complete cds"; | | |
| RL | Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; AB19212; BAD5486.1; -; mRNA. | FT | CHAIN SIGNAL 1 15 |
| DR | GO; GO:0007596; P:blood coagulation; IBA. | FT | CHAIN 16 >981 |
| DR | InterPro; IPR02181; Fibrinogen_C. | FT | DOMAIN 283 >481 |
| DR | PFam; PF00147; Fibrinogen_C; 1. | FT | COILED COIL 153 261 |
| DR | SMART; SM00186; FBG; 1. | FT | CARBONYL 92 92 |
| DR | PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. | FT | Glycoprotein; SIGNAL 1 15 |
| DR | PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. | FT | CARBONYL 122 122 |
| SEQUENCE | 497 AA; 57415 MW; 061AFC2B038F081 CRC64; | FT | N-Linked (GLCNAC. . .) (Potential). |
| SQ | . | FT | CARBONYL 154 154 |
| Query Match | Score 81.6%; DB 2; Length 497; | FT | N-Linked (GLCNAC. . .) (Potential). |
| Best Local Similarity | 90.0%; Pred. No. 0.00017; | FT | CARBONYL 243 243 |
| Matches 18; | Conservative 1; Mismatches 0; Indels 1; Gaps 1; | FT | N-Linked (GLCNAC. . .) (Potential). |
| Qy | 1 LCTKREGVLLKGKREEEKPF 20 | FT | DISULFID 294 294 |
| Db | 264 LCTKE-VLLKGKREEEKPF 282 | FT | DISULFID 285 314 |
| | | FT | DISULFID 438 451 |
| | | FT | NON_TER 481 481 |
| | | SEQUENCE | 55557 MW; 88ECB8D84FC2B2B50 CRC64; |
| RESULT 12 | | | |
| ID | ANGP1_BOVIN | | |
| STANDARD; | | | |
| PRT; | | | |
| Score 85.5; | | | |
| DB 1; | | | |
| Length 481; | | | |
| Best Local Similarity 90.0%; | | | |
| Prod. No. 0.00024; | | | |
| Matches 18; | | | |
| Conservative 1; | | | |
| Mismatches 0; | | | |
| Indels 1; | | | |
| Gaps 0; | | | |

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISSA) system 384 format sequencing pipeline with 384 multiplex capillary sequencer.", Genome Res. 10:1757-1771 (2000).

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC CAAE01015010; CAG09974.1; -; Genomic_DNA.

DR InterPro; IPR011700; BZIP_2.

DR InterPro; IPR04827; TF_bZIP_2.

DR Pfam; PF07716; BZIP_2_1.

DR PROSITE; PS00217; BZIP_1.

DR PROSITE; PS00036; BZIP_BASIC_1.

DR DNA-binding; Nuclear_protein.

SQ SEQUENCE 178 AA; 19157 MW; 832C61408C134DCP CRC64;

Query Match 51.9%; Score 55; DB 2; Length 178;

Best Local Similarity 55.6%; Pred. No. 4.1;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0.

Qy 2 CTKBEGVLLKGKREEK 19

Db 4 CTKBEGVLLKGKREEK 21

Search completed: December 29, 2005, 15:40:14

Job time : 233 secs

Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.

EMBL; AK015458; BAB29870.2; -, mRNA.

DR Ensemble; ENSMUSG0000024280; Mus musculus.

MG1; MG1:1922:84; PRMC4.

KW Hypothetical protein.

PT 383 AA; 43608 MW; AA688BA4AACB01D CRC64;

SEQUENCE 383 AA; 43608 MW; AA688BA4AACB01D CRC64;

Query Match 55.7%; Score 59; DB 2; Length 383;

Best Local Similarity 68.8%; Pred. No. 2.1;

Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0.

Qy 2 CTKBEGVLLKGKREE 17

Db 262 CTKBEGVLLKGKREE 277

RESULT 15

Q4RNQ8 TETNG PRELIMINARY; PRT; 178 AA.

ID Q4RNQ8_TETNG PRELIMINARY;

AC Q4RNQ8;

DT 13-SEP-2005 (TREMBrel. 31, Created)

DT 13-SEP-2005 (TREMBrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBrel. 31, Last annotation update)

DE ORFnames=GSTBNG00031451001;

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Noteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetradontoidae; Tetraodontidae; Tetraodon.

NCBI_TAXID=99883;

[1] -

RN NUCLEOTIDE SEQUENCE.

RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Cozar C., Bernot A., Nicaud S., Jaffre D., Fisher S., Lutfalla G., Dobsat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biémont C., Skalli Z., Cattolico L., Poulat J., De Bernardinis V., Crusaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan P., McEwan P., Bosak S., Kellis M., Vollif JN., Guigo R., Zody M.C., Masirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quétier F., Sturin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H., "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.", Nature 431:946-957 (2004).

RT RL

OTHER INFORMATION: 2N1C1F (chimera 4)

Query Match Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKREEEKPF 20
Db 261 LCTKEGVLLKGKREEEKPF 280

RESULT 6

US-10-225-060-26

; Sequence 26, Application US/1025060

; Patent No. 6825008

; GENERAL INFORMATION:

; APPLICANT: Davis et al.

; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling

; FILE REFERENCE: REG 333-2

CURRENT APPLICATION NUMBER: US/10/225.060

PRIOR FILING DATE: 2002-08-21

PRIOR APPLICATION NUMBER: US/09/709,188

PRIOR FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 08/740,223

PRIOR FILING DATE: 1996-10-25

SOFTWARE: PatentIn version 3.1

SEQ ID NO 26

LENGTH: 495

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Chimeric

FEATURE:

OTHER INFORMATION: 2N1C1F (chimera 4)

US-10-225-060-26

Query Match Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKREEEKPF 20
Db 261 LCTKEGVLLKGKREEEKPF 280

RESULT 7

US-08-740-223A-14

; Sequence 14, Application US/08740223A

; Patent No. 6265564

; GENERAL INFORMATION:

; APPLICANT: Davis, et al.

; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule

; NUMBER OF SEQUENCES: 28

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill Road

CITY: Tarrytown

STATE: NY

COUNTRY: USA

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

APPLICATION NUMBER: US/08/740,223A

FILING DATE: 25-OCT-1996

CLASSIFICATION: 536

PRIOR FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: 08/740,223
 PRIOR FILING DATE: 1996-10-25
 NUMBER OF SEQ ID NOs: 30
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 14
 LENGTH: 497
 TYPE: PRT
 ORGANISM: Mus sp.
 US-10-225-060-14

Query Match 100.0%; Score 106; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20
 Db 264 LCTKEGVLLKGGRREEKPF 283

RESULT 11
 US-08-418-595-2
 Sequence 2, Application US/08418595
 Patent No. 5814464
 GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill River Road
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/418,595
 FILING DATE: 06-APR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/373,579
 FILING DATE: 17-JAN-1995
 APPLICATION NUMBER: US 08/353,503
 FILING DATE: 09-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/373,579
 FILING DATE: 17-JAN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/353,503
 FILING DATE: 09-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,492
 FILING DATE: 02-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/330,261
 FILING DATE: 27-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/319,932
 FILING DATE: 07-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Cobert, Robert J.
 REGISTRATION NUMBER: 36,108
 REFERENCE/DOCKET NUMBER: REG 330-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 345-7400
 TELEFAX: (914) 345-7721
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-418-595-2

Query Match 100.0%; Score 106; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20
 Db 264 LCTKEGVLLKGGRREEKPF 283

RESULT 12
 US-08-665-926-2

Query Match 100.0%; Score 106; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20
 Db 264 LCTKEGVLLKGGRREEKPF 283